

FT	Modified-site	78..84	/label= Tyrosine_kinase_phosphorylation_site
FT	Region	96..125	/label= Myelin_PO_protein
FT	Modified-site	106..109	/note= "Asn is N-glycosylated"
FT	Domain	155..214	/label= Immunoglobulin_domain
FT	Modified-site	201..204	/note= "Asn is N-glycosylated"
FT	Region	229..283	/label= Myelin_PO_protein
FT	Domain	231..256	/label= Transmembrane_domain
FT	Modified-site	262..269	/label= Tyrosine_kinase_phosphorylation_site
FT	Modified-site	298..301	/note= "Asn is N-glycosylated"
PN	WO200116319-A2.		
XX	08-MAR-2001.		
XX	23-AUG-2000; 2000WO-US23522.		
XX	31-AUG-1999; 99US-0151733.		
PR	01-SEP-1999; 99WO-US20111.		
PR	16-DEC-1999; 99WO-US03095.		
PR	18-FEB-2000; 2000WO-US04342.		
PR	01-MAR-2000; 2000WO-US05601.		
PR	30-MAR-2000; 2000WO-US08439.		
PR	17-MAY-2000; 2000WO-US13705.		
PR	22-MAY-2000; 2000WO-US14042.		
PR	30-MAY-2000; 2000WO-US1941.		
PR	05-JUN-2000; 2000US-0209832.		
PA	(GETH) GENENTECH INC.		
PI	Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Tumas D,		
PI	Watanabe CK, Wood WI;		
XX	WPI: 2001-226690/23.		
DR	N-PESDB; AAD02924.		
XX			
PT	New PRO polypeptides for treating immune related and inflammatory		
PT	diseases such as rheumatoid arthritis, systemic vasculitis, asthma,		
PT	autoimmune hemolytic anemia, and diabetes mellitus		
XX			
PS	Claim 10; Fig 10; 118pp; English.		
XX			
CC	The present sequence is PRO5723 protein encoded by DNA82361 cDNA		
CC	clone. PRO protein, its agonist or antagonist or its antibody which are		
CC	capable of enhancing or inhibiting the proliferation of T-lymphocytes		
CC	or of increasing the infiltration of inflammatory cells into a tissue		
CC	are useful in the diagnosis and treatment of immune-related diseases		
CC	in mammals. The PRO protein is useful for treating systemic lupus		
CC	erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic		
CC	arthritis, spondyloarthritis, systemic sclerosis, idiopathic		
CC	inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,		
CC	sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia		
CC	thyroiditis, diabetes mellitus, immune-mediated renal disease,		
CC	demyelinating disease of the central or peripheral nervous system,		
CC	idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,		
CC	chronic inflammatory demyelinating polyneuropathy, hepatobiliary		
CC	disease, infectious or autoimmune chronic active hepatitis, primary		
CC	biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,		
CC	inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's		
CC	disease, autoimmune or immune-mediated skin diseases such as bullous		
CC	skin disease, erythema multiforme and contact dermatitis, psoriasis,		
CC	allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,		
CC	food hypersensitivity and urticaria, immunologic diseases of the lung		
CC	such as eosinophilic pneumonia, idiopathic pulmonary fibrosis, hyper-		
CC	sensitivity pneumonitis, transplantation associated diseases such as		

CC	graft rejection or graft-versus-host-disease.
XX	Sequence 352 AA;
XX	Query Match 91.1%; Score 1238; DB 22; Length 352;
XX	Best Local Similarity 89.3%; Pred. No. 2,4e-108;
XX	Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
QY	1 MALLCFLVLLCGVADLTRSLSTTPEOMIEKAGETAYLPCRFLLGPDGQPLDIEMWLS 60
DB	1 MALLCFLVLLCGVADFPARSLSTTPEBEMIKAGETAYLPCCKFTLLSPEDGQPLDIEMWLS 60
QY	61 PADNQRKDYVITIIYXSGKRTDPDYODLKGKVFHTSNLKSGDASINVTNLQSLDIGYQC 120
DB	61 PADNQRKDYVITIIYXSGKRTDPDYODLKGKVFHTSNLKSGDASINVTNLQSLDIGYQC 120
QY	121 KVKKAPGAVGNKKIQLTVLLKPSGTRCYVDGSEETIGNDFPKLCEPKESGLPLLEYQKLSN 180
DB	121 KVKKAPGAVGNKKIHLVVLVVKPSGARCYVDGSEETIGSFPIKCEPKESGLPLQYEMQKLSN 180
QY	181 SQKLPITLMAEMTSVPVISVKNASTEYSGTYSCTVKNRVGSDQCLRLDVPVPPSNRAGTIA 240
DB	181 SQKRPFTLMAEMTSVVISVKNASSEYSGTYSCTVRNRVGSQDCLRLNVPVPPSNKAGLIA 240
QY	241 GAVIGVLLALVILGILIFCCR 261
DB	241 GAVIGVLLALVILGILIFCCR 261
RESULT 2	
AAB65294	
ID	AAB65294 standard; Protein; 352 AA.
XX	
AC	AAB65294;
DT	02-APR-2001 (first entry)
XX	
DE	Human PRO5723 protein sequence SEQ ID NO:505.
XX	
KM	Human; secreted and transmembrane protein; PRO; cytosstatic;
KW	cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
XX	diagnostic assay.
OS	Homo sapiens.
XX	
PN	WO200073454-A1.
XX	
PD	07-DEC-2000.
XX	
PF	30-MAR-2000; 2000WO-US08439.
XX	
XX	02-JUN-1999; 99WO-US12252.
PR	23-JUN-1999; 99US-0141037.
PR	07-JUL-1999; 99US-0143048.
PR	20-JUL-1999; 99US-0144758.
PR	26-JUL-1999; 99US-0145698.
PR	28-JUL-1999; 99US-0146222.
PR	17-AUG-1999; 99US-0149396.
PR	15-SEP-1999; 99WO-US21090.
PR	15-SEP-1999; 99WO-US21547.
PR	08-OCT-1999; 99US-0158663.
PR	30-NOV-1999; 99WO-US28301.
PR	01-DEC-1999; 99WO-US28301.
PR	16-DEC-1999; 99WO-US30095.
PR	20-DEC-1999; 99WO-US30911.
PR	03-JAN-2000; 2000WO-US00219.
PR	06-FEB-2000; 2000WO-US00376.
PR	11-FEB-2000; 2000WO-US03565.
PR	18-FEB-2000; 2000WO-US04341.
PR	22-FEB-2000; 2000WO-US04414.
PR	24-FEB-2000; 2000WO-US04914.
PR	24-FEB-2000; 2000WO-US05004.
PR	02-MAR-2000; 2000WO-US05841.

PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PA (GENTH) GENENTECH INC.
 PI Ashkenazi AJ, Baker KP, Boltschein D, Desnoyers L, Eaton DL,
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi CJ, Gurney AL, Kijavini IU, Napier MA, Pan J, Paoni NF,
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
 PI Zhang Z;
 DR MPI: 2001-032160/04.
 DR N-PSDB; AAF44263.
 PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 318; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytosolic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAF65154 to AAF65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SO Sequence 352 AA:
 Query Match 91.1%; Score 1238; DB 22; Length 352;
 Best Local Similarity 89.3%; Pred. No. 2.4e-108;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MALLLCFVLLCGVADLTSLSTTPPEOMTEKAGETAYLPCCRTTLPEDQGPDIEMWLS 60
 DB 1 MALLLCFVLLCGVADLTSLSTTPPEOMTEKAGETAYLPCCRTTLPEDQGPDIEMWLS 60
 QY 61 PADNOKVDPVVIILYSGDKTYDDYDYLKGRVHTSNDLSGASINVTNLQSLDGTGTC 120
 DB 61 PADNOKVDPVVIILYSGDKTYDDYDYLKGRVHTSNDLSGASINVTNLQSLDGTGTC 120
 QY 121 KYKKAQGVGNKKIQLTVLKPSTGRCYVDGSEIEGDFLKCPEKGSPLLYEMOKLSN 180
 DB 121 KYKKAQGVGNKKIQLTVLKPSTGRCYVDGSEIEGDFLKCPEKGSPLLYEMOKLSN 180
 QY 121 KYKKAQGVGNKKIQLTVLKPSTGRCYVDGSEIEGDFLKCPEKGSPLLYEMOKLSN 180
 DB 121 KYKKAQGVGNKKIQLTVLKPSTGRCYVDGSEIEGDFLKCPEKGSPLLYEMOKLSN 180
 QY 181 SOKLPTLMLAEMTSPIYSVKNASTSEYSGTCTVKNRVSGDOCLLFLVDPSPNAGTIA 240
 DB 181 SOKLPTLMLAEMTSPIYSVKNASTSEYSGTCTVKNRVSGDOCLLFLVDPSPNAGTIA 240
 QY 241 GAVIGVLLALVLIIGLIIFCCR 261
 DB 241 GAVIGVLLALVLIIGLIIFCCR 261
 QY 241 GAVIGVLLALVLIIGLIIFCCR 261
 DB 241 GAVIGVLLALVLIIGLIIFCCR 261
 RESULT 3
 AAB50930
 ID AAB50930 standard; Protein; 352 AA.
 AC AAB50930;
 XX
 XX 21-MAR-2001 (first entry)
 DT Human PRO5723 protein.
 XX
 DE Human; PRO; antiinflammatory; dermatological; antiarthritic;
 KW

KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
 KW antidiabetic; nootropic; neuroprotective; hepatotropic; virocidic;
 KW anti-allergic; antiasclerotic; immune related disorder;
 KW hepatobiliary disease; autoimmune disease; allergy.
 XX
 OS Homo sapiens.
 XX
 PN WO200073452-A2.
 XX
 PD 07-DEC-2000.
 XX
 XX 02-JUN-2000; 2000WO-US15264.
 PF
 XX 02-JUN-1999; 99WO-US12252.
 PR 20-JUL-1999; 99US-0144732.
 PR 20-JUL-1999; 99US-0144758.
 PR 28-JUL-1999; 99US-0146222.
 PR 01-SEP-1999; 99WO-US20111.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28634.
 PR 09-DEC-1999; 99US-0170262.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL,
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK,
 PI Wood WI;
 XX
 DR MPI: 2001-025253/03.
 DR N-PSDB; AAC91489.
 XX
 PT Thirty three nucleic acids encoding PRO polypeptides which are useful
 PT in the diagnosis and treatment of immune related disorders, e.g.
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 PT thyroiditis and diabetes mellitus -
 XX
 PS Claim 58; Fig 58; 218pp; English.
 XX
 CC The present sequence is one of thirty three novel PRO polypeptides.
 CC The PRO polypeptides, anti-PRO antibodies, agonists and
 CC antagonists are useful for treating and diagnosing immune related
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
 CC (such as infectious, autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
 CC

CC Food hypersensitivity and urticaria), immunological diseases of the
 CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
 CC and hypersensitivity pneumonitis), transplant-associated diseases
 CC including graft rejection and graft-versus-host diseases.

XX Sequence 352 AA;

Query Match 91.1%; Score 1238; DB 22; Length 352;
 Best Local Similarity 89.3%; Pred. No. 2.4e-108;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADITRSLSTTPPEOMIEKAGETAYLPCKFTLSPEDGPIDIEMWLS 60
 DB 1 MALLLCFVLLCGVADITRSLSTTPPEOMIEKAGETAYLPCKFTLSPEDGPIDIEMWLS 60
 QY 61 PADNOKVDVITILYSGDKTYDDYODLKGKRVHFTSNDLKSASINVTNLQSLDGTGYOC 120
 DB 61 PADNOKVDVITILYSGDKTYDDYODLKGKRVHFTSNDLKSASINVTNLQSLDGTGYOC 120
 QY 121 KYKAKGVGNKKIQLTVLLKPSGTRCYVDGSEIEGDFKLKCPKESGLPLYLEMOKLSN 180
 DB 121 KYKAKGVGNKKIQLTVLLKPSGTRCYVDGSEIEGDFKLKCPKESGLPLYLEMOKLSN 180
 QY 181 SQKLPFLMLAEMTSPIVSKNASTERYSGTYSCTVKNRVGSDQCLRLDVPSPNRAQTIA 240
 DB 181 SQKLPFLMLAEMTSPIVSKNASTERYSGTYSCTVKNRVGSDQCLRLDVPSPNRAQTIA 240
 QY 241 GAVIGVLLALVILGLIIFCCR 261
 DB 241 GAVIGVLLALVILGLIIFCCR 261

RESULT 4

ABR95562 standard; Protein; 352 AA.

XX ABR95562;
 XX 19-JUL-2002 (first entry)
 DE Human angiogenesis related protein PRO5723 SEQ ID NO: 280.
 XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KM cardiatic; cytostatic; antiangiogenic; hypotensive; vulnerary;
 XX antiarteriosclerotic.
 OS Homo sapiens.
 XX MO200208284-A2.
 PD 31-JAN-2002.
 XX 09-JUL-2001; 2001WO-US21735.
 XX 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23338.
 PR 07-SEP-2000; 2000US-230978P.
 PR 15-SEP-2000; 2000US-000000P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.

PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-080889.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US00000.

XX (GETH) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERR) FERRARA N.
 PA (GERB) GERBER H.
 PA (GERR) GERRITSEN M E.
 PA (GODD) GODDARD A.
 PA (GODD) GODDARD P J.
 PA (GURN) GURNEY A L.
 PA (HILL) HILLAN K J.
 PA (MARS) MARSTERS S A.
 PA (PANJ) PAN J.
 PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P M.
 PA (WOOD) WOOD W I.

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
 DR WFI; 2002-171999/22.
 DR N-PSDB; ABL95700.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 11; Fig 280; 567pp; English.

XX The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thromboplastic, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 352 AA;

Query Match 91.1%; Score 1238; DB 23; Length 352;
 Best Local Similarity 89.3%; Pred. No. 2.4e-108;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADITRSLSTTPPEOMIEKAGETAYLPCKFTLSPEDGPIDIEMWLS 60
 DB 1 MALLLCFVLLCGVADITRSLSTTPPEOMIEKAGETAYLPCKFTLSPEDGPIDIEMWLS 60
 QY 61 PADNOKVDVITILYSGDKTYDDYODLKGKRVHFTSNDLKSASINVTNLQSLDGTGYOC 120
 DB 61 PADNOKVDVITILYSGDKTYDDYODLKGKRVHFTSNDLKSASINVTNLQSLDGTGYOC 120


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QY 121 KYKAPGVGNKKIQLTVLTKPSGTRCYVDGSEIIGNDFLTKCEPKEGSLPLLEYWOKLSN 180
DB 121 KYKAPGVGNKKIHLVVLVPSGARCVDGSEIIGSDPFKICEPKESLPLLEYWOKLSN 180
QY 181 SQKPLTLMIAEMTSPVIVSNASTSEYSGTYSCTVKNRVSGDCLRLDVPVPENRAGTIA 240
DB 181 SQKPLTLMIAEMTSPVIVSNASTSEYSGTYSCTVKNRVSGDCLRLDVPVPENRAGTIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 5
ABR84956
ID ABR84956 standard; Protein; 352 AA.
XX
AC ABR84956;
XX
DE 16-MAY-2002 (first entry)
XX
DT Human PRO5723 protein sequence SEQ ID NO:280.
XX
DE Human: angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;
XX vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
XX age-related macular degeneration; arterial restenosis; angina;
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX lymphangitis; tumor angiogenesis; breast carcinoma; liver carcinoma;
XX wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
XX WO200200690-A2.
XX
PD 03-JUN-2002.
XX
PF 20-JUN-2001; 2001WO-US19692.
XX
XX 23-JUN-2000; 2000US-213637P.
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220664P.
XX 28-JUL-2000; 2000WO-US20710.
XX 02-AUG-2000; 2000US-222695P.
XX 17-AUG-2000; 2000US-0643657.
XX 23-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 07-SEP-2000; 2000US-230978P.
XX 18-SEP-2000; 2000US-0664610.
XX 18-SEP-2000; 2000US-0665350.
XX 24-OCT-2000; 2000US-242922P.
XX 08-NOV-2000; 2000US-0709238.
XX 08-NOV-2000; 2000WO-US30952.
XX 10-NOV-2000; 2000WO-US30873.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 22-JAN-2001; 2001US-0767609.
XX 28-FEB-2001; 2001US-0796498.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-MAR-2001; 2001WO-US06666.
XX 09-MAR-2001; 2001US-0802706.
XX 14-MAR-2001; 2001US-0808689.
XX 22-MAR-2001; 2001US-0816744.
XX 05-APR-2001; 2001US-0828366.
XX 10-MAY-2001; 2001US-0854208.
XX 10-MAY-2001; 2001US-0854280.
XX 25-MAY-2001; 2001US-0866028.
XX 25-MAY-2001; 2001US-0866034.
XX 25-MAY-2001; 2001WO-US17092.
XX 30-MAY-2001; 2001US-0870574.

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PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX
XX (GETH ) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gueney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
PI Stephan UF, Watanabe CK, Williams PW, Wood WI, Ye W,
XX WPI; 2002-090516/12.
XX DR N-PSDB; ABL88211.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorder in a mammal -
XX
PS Claim 11; Fig 280; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABR84817 to
XX ABR85003. The PRO proteins and polynucleotides have cardiac, cytostatic,
XX antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX a cardiovascular, endothelial or angiogenic disorder in a mammal,
XX e.g. cardiac hypertrophy, trauma, cancer, age-related macular
XX degeneration, atherosclerosis, hypertension, arterial restenosis,
XX rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
XX CC lymphangitis, tumor angiogenesis (such as breast carcinoma and liver
XX carcinoma) and wound healing. The PRO polynucleotides have applications
XX in molecular biology including use as hybridisation probes, and in
XX CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
XX CC probes used in the exemplification of the present invention.
XX
SQ Sequence 352 AA;
XX
XX Query Match 91.1%; Score 1238; DB 23; Length 352;
XX Best Local Similarity 89.3%; Pred. No. 2.4e-108;
XX Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
XX
QY 1 MALLLCFVLLCGVADLTRSLSTTPPEOMTEKAGETAYVPCRFLLGPEDQGPDIEMWLS 60
DB 1 MALLLCFVLLCGVADTRSLSTTPPEOMTEKAGETAYVPCRFLLGPEDQGPDIEMWLS 60
QY 61 PADNOKVDVITLLYSGDKYDDYDYLKGRVFTSNDLKSGBASINVTNLQSDIGTYOC 120
DB 61 PADNOKVDVITLLYSGDKYDDYDYLKGRVFTSNDLKSGBASINVTNLQSDIGTYOC 120
QY 121 KYKAPGVGNKKIQLTVLTKPSGTRCYVDGSEIIGNDFLTKCEPKEGSLPLLEYWOKLSN 180
DB 121 KYKAPGVGNKKIHLVVLVPSGARCVDGSEIIGSDPFKICEPKESLPLLEYWOKLSN 180
QY 181 SQKPLTLMIAEMTSPVIVSNASTSEYSGTYSCTVKNRVSGDCLRLDVPVPENRAGTIA 240
DB 181 SQKPLTLMIAEMTSPVIVSNASTSEYSGTYSCTVKNRVSGDCLRLDVPVPENRAGTIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 6
AAM69697
ID AAM69697 standard; Protein; 365 AA.
XX
AC AAM69697;
XX
DT 07-DEC-1998 (first entry)
XX
DE Human coxsackievirus and Ad2 and Ad5 receptor HCAR protein.
XX
DE HCAR, coxsackievirus receptor; CVB; adenovirus; Ad2 receptor;
XX KW Ad5 receptor; human; infection; vaccine; therapy.
XX
XX

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OS Homo sapiens.
XX Key Location/Qualifiers
FH Domain 35..130
FT /note= "extracellular immunoglobulin domain"
FT 155..220
FT Domain /note= "extracellular immunoglobulin domain"
FT 45..52
FT Region /note= "CVB binding region (Claim 6)"
FT 47..51
FT Region /note= "Ad2/5 and CVB binding region (Claim 6)"
FT 53..57
FT Region /note= "Ad2/Ad5 binding region (Claim 6)"
FT 69..73
FT Region /note= "Ad2/Ad5 binding region (Claim 6)"
FT 72..77
FT Region /note= "Ad2/5 and CVB binding region (Claim 6)"
FT 72..77
FT Region /note= "CVB-binding region (Claim 6)"
FT 77..79
FT Region /note= "Ad2/Ad5 binding region (Claim 6)"
FT 96..100
FT Region /note= "CVB-binding region (Claim 6)"
FT 122..127
FT Region /note= "Ad2/5 and CVB binding region (Claim 6)"
FT /note= "Ad2/5 and CVB binding region (Claim 6)"

MO9833819-A1.
XX
XX 06-AUG-1998.
XX 30-JAN-1998; 98WO-US01724.
XX 30-JAN-1997; 97US-0036986.
XX (UYNV ) UNIT NEW YORK STATE.
XX
XX Philipson L, Tomko RP.
XX
XX WPI; 1998-437397/37.
XX N-PSDB; AAV50429.
XX
XX DNA encoding human receptor for adenovirus C and coxsackievirus B -
XX PT for preventing and treating viral infection and rendering cells
XX PT susceptible to transformation by adenoviral vectors in gene therapy
XX
XX Claim 3; Page 67-68; 88pp; English.
XX
XX This is the amino acid sequence of human HCAR, a protein that
XX CC serves as a cellular receptor for adenoviruses of the serotypes 2
XX CC and 5 (subgroup C) and for the group B coxsackieviruses (CVB). The
XX CC sequence was deduced from an isolated cDNA clone for HCAR (see
XX CC AAV50429). The invention also provides host cells transformed with
XX CC DNA molecules encoding HCAR or mouse mCAR (see AAM69698) and methods
XX CC of producing the recombinant proteins or their derivatives. These
XX CC proteins, their extracellular domains, as well as oligopeptides
XX CC (see AAM69699-708) which bind virus, are claimed. Isolated HCAR or
XX CC mCAR proteins or their fragments or variants are used to prevent or
XX CC treat virus infections and for inhibiting the infectivity of Ad2,
XX CC Ad5 or CVB. Methods are also provided for detecting or measuring
XX CC the quantity of HCAR or mCAR in a sample, and for identifying
XX CC analytes capable of binding to HCAR or mCAR.
XX
XX Sequence 365 AA;
XX
XX Query Match 91.1%; Score 1238; DB 19; Length 365;
XX Best Local Similarity 89.3%; Pred. No. 2.6e-108;
XX Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
XX
XX 1 MALLLCFVLLCGVADLRSLSTTPPEOMIKAKGETYVLCRFTGPDGSPDLIDIELLS 60
XX 1 MALLLCFVLLCGVADLRSLSTTPPEOMIKAKGETYVLCRFTGPDGSPDLIDIELLS 60
XX 1 MALLLCFVLLCGVADLRSLSTTPPEOMIKAKGETYVLCRFTGPDGSPDLIDIELLS 60
XX 61 PADNOKVDOYIILVSGDKIYDDYVDLKGKGVHFTSNDLKSQDASINVTNLQLSDIGTYQC 120

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DB 61 PADNOKVDOYIILVSGDKIYDDYVDLKGKGVHFTSNDLKSQDASINVTNLQLSDIGTYQC 120
QY 121 KYKAPGVGNKKIQTLLVLLKPSGTRCYVDGSEIEIGNDFLKCEPKEGSLPLYEMOKLSN 180
DB 121 KYKAPGVGNKKIHLVLLVLPKPGARCYVDGSEIEIGNDFLKCEPKEGSLPLYEMOKLSN 180
QY 181 SQKLPFLWLAEMTSPVSVKNASSTEGSYCTVKNRVSSDCLRLDVPVPSNAGTIA 240
DB 181 SQKLPFLWLAEMTSPVSVKNASSTEGSYCTVKNRVSSDCLRLDVPVPSNAGTIA 240
QY 241 GAVIGVLLALVLLGLIFCCR 261
DB 241 GAVIGVLLALVLLGLIFCCR 261

RESULT 7
AAM57212
ID AAM57212 standard; Protein, 365 AA.
XX
XX AAM57212;
XX
XX 03-AUG-1998 (first entry)
XX
XX Human coxsackievirus and adenovirus receptor.
XX
XX Human; coxsackievirus; adenovirus; receptor; CAR; cardiac infection;
XX KW myocarditis; pericarditis; dilated cardiomyopathy; meningoencephalitis;
XX KW pancreatic infection; acute pancreatitis; gastrointestinal tract;
XX KW diabetes mellitus.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH MISC-difference 188
FT /note= "encoded by TCG"
XX
XX MO9811221-A2.
XX
XX 19-MAR-1998.
XX
XX 12-SEP-1997; 97WO-US16189.
XX 13-SEP-1996; 96US-0026100.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX
XX Bergelson JM, Finberg RW, Horowitz MS;
XX
XX WPI; 1998-207384/18.
XX N-PSDB; AAV28845.
XX
XX DNA encoding coxsackie virus and adenovirus receptor - useful for
XX PT modulation of e.g. cardiac, pancreatic or gastrointestinal infection
XX
XX Claim 12; Fig 1B; 104pp; English.
XX
XX The present sequence represents human coxsackievirus and adenovirus
XX CC receptor (CAR). The present invention also describes: (1) a method for
XX CC modulating CAR expression comprising contacting the cell with an agent
XX CC which modulates CAR protein activity or CAR nucleic acid expression,
XX CC such that a cell associated activity is altered relative to a cell
XX CC associated activity of the cell in the absence of the agent; and (2) a
XX CC method for detecting the presence of CAR in a biological sample
XX CC comprising contacting a biological sample with an agent capable of
XX CC detecting CAR protein or mRNA such that the presence of CAR is detected.
XX CC Modulation of CAR is useful for treatment of cardiac infection, e.g.
XX CC myocarditis, pericarditis or dilated cardiomyopathy, or infection of the
XX CC central nervous system, e.g. a non-specific febrile illness or
XX CC meningoencephalitis, or pancreatic infection, e.g. acute pancreatitis,
XX CC or infection of the respiratory or gastrointestinal tract or childhood
XX CC onset diabetes mellitus. Probes derived from CAR nucleic acids are
XX CC useful for hybridisation assays, and antibodies raised against CAR

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CC protein are useful for blocking CAR expression. Cell-free assays which
CC include combining CAR protein and a candidate/test compound are useful
CC in screening for drugs which interact with CAR protein.

XX Sequence 365 AA;

Query Match 91.1%; Score 1238; DB 19; Length 365;
Best Local Similarity 89.3%; Pred. No. 2.6e-108;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLCFVLLCGVADLTSLSTTPEOMTEKAKGTAYLPCEFTLGPEPDGDLIDEMLS 60
DB 1 MALLCFVLLCGVADLTSLSTTPEOMTEKAKGTAYLPCEFTLGPEPDGDLIDEMLS 60
QY 61 PADNOKVDQVILLYSGDKIYDDYODLKGKRVHFTSNDLKSASPASINVTNLQSDIGTYOC 120
DB 61 PADNOKVDQVILLYSGDKIYDDYODLKGKRVHFTSNDLKSASPASINVTNLQSDIGTYOC 120
QY 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDSSEIENDFKLCEPKEGSLPLLYEMOKLSN 180
DB 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDSSEIENDFKLCEPKEGSLPLLYEMOKLSN 180
QY 181 SOKLPTLWLAEMTSVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVVPPSNRAGTIA 240
DB 181 SOKLPTLWLAEMTSVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVVPPSNRAGTIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 8
AAB47270
ID AAB47270 standard; Protein; 365 AA.

XX AAB47270;

DT 06-AUG-2001 (first entry)

DE Human CAR.

KM Coxsackie virus and/or Adenovirus receptor; CAR; transgenic mouse;
KW transgene; tCAR; transduction; integrin; gene transfer; lymphocyte;
XX lymphocyte-specific transcription regulatory sequence; T cell.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Protein 1..262

XX /note= "Claimed tCAR"

PN US6245966-B1.

PD 12-JUN-2001.

PF 19-MAR-1999; 99US-0272496.

PR 14-JUL-1998; 98US-0092782.

PA (UYTE-) UNIV TECHNOLOGY CORP.

PI DeGregori J;

DR MPI; 2001-366549/38.

DR N-PSDB; AAC85813.

PT Transgenic mouse comprising a nucleotide sequence encoding a truncated
PT Coxsackie virus and/or Adenovirus receptor (tCAR) polypeptide useful for
PT the analysis of cellular physiology -

PS Claim 3; Column 15-18; 21pp; English.

XX This sequence shows a Coxsackie virus and/or Adenovirus receptor (CAR)

CC polypeptide. The DNA encoding this sequence was used in the method of
CC the invention to produce a transgenic mouse whose genome comprises a
CC transgene comprising a nucleotide sequence encoding a truncated CAR
CC polypeptide (tCAR) operably linked to a lymphocyte-specific
CC transcription regulatory nucleotide sequence. The tCAR is expressed
CC in the lymphocytes of the mouse at levels sufficient for increased
CC susceptibility to adenoviral transduction of the lymphocytes without
CC affecting the expression of endogenous integrins in the lymphocytes.

CC The transgenic mouse is useful for the analysis of pathways, via gene
CC transfer, which control various aspects of cellular physiology either
CC in vitro or in vivo. The tCAR-regulatory sequence construct facilitates
CC either the in vivo delivery of genes into T cells by the inoculation of
CC adenovirus recombinants into lymphoid organs or the ex vivo delivery of
CC genes into transgenic T cells as T cells expressing the truncated form
CC of tCAR are highly efficient target cells for adenoviral transduction.

XX Sequence 365 AA;

Query Match 91.1%; Score 1238; DB 22; Length 365;
Best Local Similarity 89.3%; Pred. No. 2.6e-108;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLCFVLLCGVADLTSLSTTPEOMTEKAKGTAYLPCEFTLGPEPDGDLIDEMLS 60
DB 1 MALLCFVLLCGVADLTSLSTTPEOMTEKAKGTAYLPCEFTLGPEPDGDLIDEMLS 60
QY 61 PADNOKVDQVILLYSGDKIYDDYODLKGKRVHFTSNDLKSASPASINVTNLQSDIGTYOC 120
DB 61 PADNOKVDQVILLYSGDKIYDDYODLKGKRVHFTSNDLKSASPASINVTNLQSDIGTYOC 120
QY 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDSSEIENDFKLCEPKEGSLPLLYEMOKLSN 180
DB 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDSSEIENDFKLCEPKEGSLPLLYEMOKLSN 180
QY 181 SOKLPTLWLAEMTSVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVVPPSNRAGTIA 240
DB 181 SOKLPTLWLAEMTSVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVVPPSNRAGTIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 9
ABB08040
ID ABB08040 standard; Protein; 365 AA.

XX ABB08040;

DT 27-AUG-2002 (first entry)

DE Human coxsackie-adenovirus receptor (CAR).

KM Targeting molecule; adenoviral receptor domain; trimerisation; cancer;
KW coxsackie-adenovirus receptor; CAR; transmembrane protein; cytoskeletal;
XX hepatotropic; virucide; gene therapy; human; receptor.

OS Homo sapiens.

XX WO200229072-A2.

PN 11-APR-2002.

PF 05-OCT-2001; 2001WO-EP11514.

PR 06-OCT-2000; 2000US-327562P.

PR 06-OCT-2000; 2000US-0684552.

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Kim JG, Smith T, Stevenson SC, Kaleko M;

DR WPI; 2002-471317/50.
 DR N-PSDB; ABL60622.
 XX
 PT A targeting molecule for use in forming complexes to treat cancer, such
 PT as adenocarcinoma of the prostate, comprises a soluble adenoviral
 PT receptor domain, a trimerization domain and a targeting ligand domain -
 XX
 PS Example 14; Page 47; 75pp; English.
 XX
 CC The invention relates to a targeting molecule that comprises a soluble
 CC adenoviral receptor domain, a trimerization domain and a targeting ligand
 CC domain. The targeting molecules are used for targeting an adenoviral
 CC particle to a cell expressing a cell surface molecule. The method
 CC involves contacting the adenoviral particle with the targeting molecule
 CC to form a complex, and contacting the cell with the complex, and in
 CC delivering a heterologous gene selectively to a cell. The complex is used
 CC for preparing a medicament for treatment of disease in a human mammal,
 CC such as cancer, preferably, adenocarcinoma of the prostate, by gene
 CC therapy. The present sequence represents the human coxsackie-adenovirus
 CC receptor (CAR), a 46 kDa transmembrane protein. The soluble form of CAR
 CC (sCAR) can be used in the targeting molecule of the invention.
 CC
 SO Sequence 365 AA;
 Query Match 91.1%; Score 1238; DB 23; Length 365;
 Best Local Similarity 89.3%; Pred. No. 2.6e-108;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MALLTCFVLICGVADLTRSLSTTPPEOMIKAGETAYLPCEFTLGPEDGPDIDIEWLIS 60
 DB 1 MALLTCFVLICGVADTFARSLSTTPPEMIKAGETAYLPCKFTLSPEDGPDIDIEWLIS 60
 QY 61 PADNOKVDVYIIYSGDKIYDDYODLKGKRVHFTSNDLKSAGSINVTNLQSLDIGTYOC 120
 DB 61 PADNOKVDVYIIYSGDKIYDDYODLKGKRVHFTSNDLKSAGSINVTNLQSLDIGTYOC 120
 QY 121 KYKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIEGDFLKCPEKSGSLPLYEMOKLSN 180
 DB 121 KYKKAPGVGNKKIHLVLLVPSGARCVDSSEIEGDFLKCPEKSGSLPLYEMOKLSN 180
 QY 181 SQKLPFLMLAEMTSPIVSVKNASTESGYTSCVKNRVSGDQCLRLDVVPPSNRAGTIA 240
 DB 181 SQKLPFLMLAEMTSPIVSVKNASTESGYTSCVKNRVSGDQCLRLDVVPPSNRAGTIA 240
 QY 241 GAVIGVLLALVILGLIIFCCR 261
 DB 241 GAVIGVLLALVILGLIIFCCR 261
 RESULT 10
 AAM69698
 ID AAM69698 standard; Protein: 352 AA.
 AC AAM69698;
 XX
 DT 07-DEC-1998 (first entry)
 XX
 DE Mouse coxsackievirus and Ad2 and Ad5 receptor MCAR protein.
 XX
 KW MCAR; coxsackievirus receptor; CVB; adenovirus; Ad2 receptor;
 KW Ad5 receptor; mouse; infection; vaccine; therapy.
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Domain 35..130
 FT /note= "extracellular immunoglobulin domain"
 FT Domain 155..220
 FT /note= "extracellular immunoglobulin domain"
 FT Region 45..52
 FT /note= "CVB binding region (Claim 6)"
 FT Region 47..51
 FT /note= "Ad2/5 and CVB binding region (Claim 6)"

FT Region 53..57
 FT /note= "Ad2/Ad5 binding region (Claim 6)"
 FT Region 69..73
 FT /note= "Ad2/Ad5 binding region (Claim 6)"
 FT Region 72..77
 FT /note= "Ad2/5 and CVB binding region (Claim 6)"
 FT Region 72..77
 FT /note= "CVB-binding region (Claim 6)"
 FT Region 77..79
 FT /note= "Ad2/Ad5 binding region (Claim 6)"
 FT Region 95..100
 FT /note= "CVB-binding region (Claim 6)"
 FT Region 122..127
 FT /note= "Ad2/5 and CVB binding region (Claim 6)"
 PN W09833819-A1.
 PD 06-AUG-1998.
 XX 30-JAN-1998; 98WO-US01724.
 PF 30-JAN-1997; 97US-0036986.
 PR (UANY) UNIT NEW YORK STATE.
 PA Philipson L, Tomko RP;
 PI WPI; 1998-437397/37.
 DR N-PSDB; AAV50430.
 XX
 XX
 PT DNA encoding human receptor for adenovirus C and coxsackievirus B -
 PT for preventing and treating viral infection and rendering cells
 PT susceptible to transformation by adenoviral vectors in gene therapy
 XX
 PS Claim 3; Page 70-71; 88pp; English.
 XX
 CC This is the amino acid sequence of mouse MCAR, a protein that
 CC serves as a cellular receptor for adenoviruses of the serotypes 2
 CC and 5 (subgroup C) and for the group B coxsackieviruses (CVB). The
 CC sequence was deduced from an isolated cDNA clone for MCAR (see
 CC AAV50430). The invention also provides host cells transformed with
 CC DNA molecules encoding MCAR or human HCAR (see AAM69697) and methods
 CC of producing the recombinant proteins or their derivatives. These
 CC proteins, their extracellular domains, as well as oligopeptides
 CC (see AAM69699-708) which bind virus, are claimed. Isolated HCAR or
 CC MCAR proteins or their fragments or variants are used to prevent or
 CC treat virus infections and for inhibiting the infectivity of Ad2,
 CC Ad5 or CVB. Methods are also provided for detecting or measuring
 CC the quantity of HCAR or MCAR in a sample, and for identifying
 CC analytes capable of binding to HCAR or MCAR.
 CC
 SO Sequence 352 AA;
 Query Match 89.5%; Score 1216; DB 19; Length 352;
 Best Local Similarity 88.1%; Pred. No. 2.9e-106;
 Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;
 QY 1 MALLTCFVLICGVADLTRSLSTTPPEOMIEKAGETAYLPCEFTLGPEDGPDIDIEWLIS 60
 DB 1 MALLTCFVLICGVADTSGTSTTPPEORIEKAGETAYLPCKFTLSPEDGPDIDIEWLIS 60
 QY 61 PADNOKVDVYIIYSGDKIYDDYODLKGKRVHFTSNDLKSAGSINVTNLQSLDIGTYOC 120
 DB 61 PSDNOKVDVYIIYSGDKIYDNYPPDLKGRVHFTSNDVKSAGSINVTNLQSLDIGTYOC 120
 QY 121 KYKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIEGDFLKCPEKSGSLPLYEMOKLSN 180
 DB 121 KYKKAPGVGNKKIQLTVLLVPSGARCVDSSEIEGDFLKCPEKSGSLPLYEMOKLSN 180
 QY 181 SQKLPFLMLAEMTSPIVSVKNASTESGYTSCVKNRVSGDQCLRLDVVPPSNRAGTIA 240
 DB 181 SQKLPFLMLAEMTSPIVSVKNASTESGYTSCVKNRVSGDQCLRLDVVPPSNRAGTIA 240

QY 241 GAVIGTLALVLIIGLIFCC 260
DB 241 GAVIGTLALVLIIGLIFCC 260

RESULT 11

ID AAM57213 standard; Protein; 376 AA.

XX AAM57213;

DT 03-AUG-1998 (first entry)

DE Mouse coxsackievirus and adenovirus receptor.

XX Mouse; coxsackievirus; adenovirus; receptor; CAR; cardiac infection;
XX myocarditis; pericarditis; dilated cardiomyopathy; meningoencephalitis;
XX pancreatic infection; acute pancreatitis; gastrointestinal tract;
XX diabetes mellitus.

OS Mus sp.

FH Key Location/Qualifiers

FT Misc-difference 366 /note="encoded by TAG, a stop codon, but the
FT sequence is shown to continue"

PN MO9811221-A2.

PD 19-MAR-1998.

XX 12-SEP-1997; 97WO-US16189.

XX 13-SEP-1996; 96US-0026100.

XX (DAND) DANA FARBER CANCER INST INC.

XX Bergelson JM, Finberg RW, Horowitz MS;

DR WPI; 1998-207384/18.

XX N-PSDB; AAV28846.

PT DNA encoding coxsackie virus and adenovirus receptor - useful for
PT modulation of e.g. cardiac, pancreatic or gastrointestinal infection

XX Disclosure; Fig 14; 104pp; English.

XX The present sequence represents mouse coxsackievirus and adenovirus
XX receptor (CAR). The present invention also describes: (1) a method for
XX modulating CAR expression comprising contacting the cell with an agent
XX which modulates CAR protein activity or CAR nucleic acid expression,
XX such that a cell associated activity is altered relative to a cell,
XX associated activity of the cell in the absence of the agent; and (2) a
XX method for detecting the presence of CAR in a biological sample
XX comprising contacting a biological sample with an agent capable of
XX detecting CAR protein or mRNA such that the presence of CAR is detected.
XX Modulation of CAR is useful for treatment of cardiac infection, e.g.
XX myocarditis, pericarditis or dilated cardiomyopathy, or infection of the
XX central nervous system, e.g. a non-specific febrile illness or
XX meningoencephalitis, or pancreatic infection, e.g. acute pancreatitis,
XX or infection of the respiratory or gastrointestinal tract or childhood
XX onset diabetes mellitus. Probes derived from CAR nucleic acids are
XX useful for hybridisation assays, and antibodies raised against CAR
XX protein are useful for blocking CAR expression. Cell-free assays which
XX include combining CAR protein and a candidate/test compound are useful
XX in screening for drugs which interact with CAR protein.

XX Sequence 376 AA;

Query Match 89.5%; Score 1216; DB 19; Length 376;
Best Local Similarity 88.1%; Pred. No. 3.2e-106;
Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTSLSTTPEQMTERAKGETATVLPCEFTLGPENQSLDIEMLLS 60
DB 1 MALLLCFVLLCGIADFTSGLSITTPFORIEKAKGETATVLPCEFTLSPEDQGLDIEMLLS 60
QY 61 PADNOKVDVILLYSGDKIYDDYODLKGKRVFTNSDLKSGDASINVTNLQJSDIGTYOC 120
DB 61 PSDNOIVDOVILLYSGDKIYDNYFPDLKGRVFTNSDLKSGDASINVTNLQJSDIGTYOC 120
QY 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFLKCPEKGSLLPLYEQKLSN 180
DB 121 KVKKAPGVANKKFLTLVLPKPSGTRCFVDGSEIIGNDFLKCPEKGSLLPLYEQKLSN 180
QY 181 SQKLEPTLWLAEMTSVYSYKNASTYSGTYSCTVKNRVSDDCLRLDVVPPSNRAGTIA 240
DB 181 SQTMPTPLWLAEMTSVYSYKNASTYSGTYSCTVKNRVSDDCLRLDVVPPSNRAGTIA 240
QY 241 GAVIGTLALVLIIGLIFCC 260
DB 241 GAVIGTLALVLIIGLIFCC 260

RESULT 12

AAU83699
ID AAU83699 standard; Protein; 290 AA.

XX AAU83699;

DT 08-MAY-2002 (first entry)

DE Human PRO protein, Seq ID No 216.

XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
XX breast cancer; prostate tumour; rectal tumour; liver tumour;
XX pericyte cell proliferation; chondrocyte cell proliferation;
XX tumour necrosis factor-alpha.

XX Homo sapiens.

XX WO200208288-A2.

XX 31-JAN-2002.

PF 29-JUN-2001; 2001WO-US21066.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220585P.

XX 25-JUL-2000; 2000US-220605P.

XX 25-JUL-2000; 2000US-220607P.

XX 25-JUL-2000; 2000US-220624P.

XX 25-JUL-2000; 2000US-220638P.

XX 25-JUL-2000; 2000US-220664P.

XX 26-JUL-2000; 2000US-220893P.

XX 28-JUL-2000; 2000WO-US20710.

XX 23-AUG-2000; 2000WO-US23522.

XX 15-SEP-2000; 2000US-000000P.

XX 10-NOV-2000; 2000WO-US30873.

XX 28-NOV-2000; 2000US-253646P.

XX 01-DEC-2000; 2000WO-US32678.

XX 20-DEC-2000; 2000US-0747259.

XX 20-DEC-2000; 2000WO-US34956.

XX 28-FEB-2001; 2001WO-US06520.

XX 10-MAY-2001; 2001US-0854280.

XX 25-MAY-2001; 2001WO-US17092.

(GETH) GENENTECH INC.

PI Baker KP, Deans J, Gerltzen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

DR WPI; 2002-172001/22.

XX N-PSDB; ABR33643.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 XX
 PS Claim 11, Figure 216; 359pp; English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AA083592-AA083713 represent human PRO
 CC protein sequences of the invention.
 XX
 SQ Sequence 290 AA;
 Query Match 86.5%; Score 1175; DB 23; Length 290;
 Best Local Similarity 89.1%; Pred. No. 1.6e-102;
 Matches 221; Conservative 13; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MALLLCFVLLCGVADLTRSLSTITPEOMIEKAGETAYLPQRFLLGPEDGPIIDIEWLIS 60
 DB 1 MALLLCFVLLCGVADFPARSLSTITPEMIEKAGETAYLPCKFTLSPEDGPIIDIEWLIS 60
 QY 61 PADNOKVDQYIILYSGDKIYDDYQDLKGRVHTSNDLKSGDASINVTNLQSLDITGYQC 120
 DB 61 PADNOKVDQYIILYSGDKIYDDYQDLKGRVHTSNDLKSGDASINVTNLQSLDITGYQC 120
 QY 121 KVKKAPGVNKKIQLTVLLKPSGRCYVDGSEIEIGNDFKICEPKKESLPLLEYMOKLSN 180
 DB 121 KVKKAPGVNKKIHLVLLKPSGARCYVDGSEIEIGDFKICEPKKESLPLLEYMOKLSN 180
 QY 181 SQKLPTLMLAEMTSPVSVKNASTREYSGTYSCTVKNRVGSDOCLRLDVPVPSNRAGTIA 240
 DB 181 SQKMPTSLAEMTSSVSVKNASSEYSGTYSCTVRNRVGSDOCLRLNVVPPSKAGALIA 240
 QY 241 GAVIGVLL 248
 DB 241 GAVIGTLL 248
 RESULT 13
 AAW82729
 ID AAW82729 standard; Protein; 264 AA.
 XX
 AC AAW82729;
 DT 29-MAR-1999 (first entry)
 XX
 DE Adenovirus PACTSG2-SCAR protein.
 XX
 KW PACTSG2-SCAR; chimeric protein; adenoviral fibre protein; monomer;
 KW trimerisation domain; affinity; substrate; gene therapy vector;
 KW attachment; interaction assay; infection.
 XX
 OS Mastadenovirus.
 OS Synthetic.
 XX
 PN WO9854346-A1.
 XX
 PD 03-DEC-1998.
 XX

PF 28-MAY-1998; 98WO-US11024.
 XX
 XX 16-JAN-1998; 98US-0071668.
 PR 28-MAY-1997; 97US-0047849.
 XX
 PA (GENV-) GENVEC INC.
 XX
 XX Brough DE, Einfeld D, Kovess I, Lizonova A, Roelink PW;
 PI Wickham TJ, Yonehiro G;
 XX
 DR WPI: 1999-059848/05.
 DR N-PSDB; AAV72025.
 XX
 XX New adenoviral fibre trimer with reduced binding to native substrate
 PT - useful for, e.g. preparing gene therapy vector with minimal
 PT ectopic infection for in vitro applications
 XX
 PS Example 8; Page 58-59; 103pp; English.
 XX
 CC This sequence represents a novel adenovirus chimeric protein,
 CC PACTSG2-SCAR. This protein is used in a method for the construction of
 CC novel monomers having an N-terminus of an adenoviral fibre protein and
 CC a trimerisation domain. Such monomers have lower affinity for native
 CC substrate than the native adenoviral fibre trimer. Cell lines containing
 CC such monomers are used (i) to propagate adenovirus for use as gene
 CC therapy vectors (for in vitro or in vivo applications), (ii) as reagents
 CC for studying adenoviral attachment and infection, and (iii) in
 CC receptor-ligand interaction assays. The new viruses produce minimal
 CC ectopic infection (they can not infect native host cells) so are safer as
 CC vectors and can be engineered for selective targeting to other cells.
 XX
 SQ Sequence 264 AA;
 Query Match 84.0%; Score 1142; DB 20; Length 264;
 Best Local Similarity 88.4%; Pred. No. 1.9e-99;
 Matches 214; Conservative 15; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MALLLCFVLLCGVADLTRSLSTITPEOMIEKAGETAYLPQRFLLGPEDGPIIDIEWLIS 60
 DB 1 MALLLCFVLLCGVADFPARSLSTITPEMIEKAGETAYLPCKFTLSPEDGPIIDIEWLIS 60
 QY 61 PADNOKVDQYIILYSGDKIYDDYQDLKGRVHTSNDLKSGDASINVTNLQSLDITGYQC 120
 DB 61 PADNOKVDQYIILYSGDKIYDDYQDLKGRVHTSNDLKSGDASINVTNLQSLDITGYQC 120
 QY 121 KVKKAPGVNKKIQLTVLLKPSGRCYVDGSEIEIGNDFKICEPKKESLPLLEYMOKLSN 180
 DB 121 KVKKAPGVNKKIHLVLLKPSGARCYVDGSEIEIGDFKICEPKKESLPLLEYMOKLSN 180
 QY 181 SQKLPTLMLAEMTSPVSVKNASTREYSGTYSCTVKNRVGSDOCLRLDVPVPSNRAGTIA 240
 DB 181 SQKMPTSLAEMTSSVSVKNASSEYSGTYSCTVRNRVGSDOCLRLNVVPPSKAGSSG 240
 QY 241 GA 242
 DB 241 GS 242
 RESULT 14
 AAW82730
 ID AAW82730 standard; Protein; 277 AA.
 XX
 AC AAW82730;
 DT 29-MAR-1999 (first entry)
 XX
 DE Adenovirus SCAR.RGD protein.
 XX
 KW SCAR.RGD; chimeric protein; adenoviral fibre protein; monomer;
 KW trimerisation domain; affinity; substrate; gene therapy vector;
 KW attachment; interaction assay; infection.
 XX
 OS Mastadenovirus.
 OS

OS Synthetic.
 XX WO9854346-A1.
 XX
 PD 03-DEC-1998.
 XX
 PF 28-MAY-1998; 98WO-US11024.
 XX
 PR 16-JAN-1998; 98US-0071668.
 PR 28-MAY-1997; 97US-0047849.
 XX
 PA (GENV-) GENVEC INC.
 XX
 PI Brough DE, Einfield D, Kovesdi I, Lizonova A, Roelvink PW;
 PI Wickham TJ, Yonehiro G;
 XX
 DR WPI: 1999-059848/05.
 DR N-PSDB; AAV72026.
 XX
 PT New adenoviral fibre trimer with reduced binding to native substrate
 PT - useful for, e.g. preparing gene therapy vector with minimal
 PT ectopic infection for in vitro applications
 XX
 PS Example 8; Page 59-60; 103pp; English.
 XX
 CC This sequence represents a novel adenovirus chimeric protein, SCAR.RGD.
 CC This protein is used in a method for the construction of novel monomers
 CC having an N-terminus of an adenoviral fibre protein and a trimerisation
 CC domain. Such monomers have lower affinity for native substrate than the
 CC native adenoviral fibre trimer. Cell lines containing such monomers are
 CC used (i) to propagate adenovirus for use as gene therapy vectors (for in
 CC vitro or in vivo applications, (ii) as reagents for studying adenoviral
 CC attachment and infection, and (iii) in receptor-ligand interaction
 CC assays. The new viruses produce minimal ectopic infection (they can not
 CC infect native host cells) so are safer as vectors and can be engineered
 CC for selective targeting to other cells.
 XX
 SQ Sequence 277 AA;
 Query Match 84.0%; Score 1142; DB 20; Length 277;
 Best Local Similarity 88.4%; Pred. No. 2e-99;
 Matches 214; Conservative 15; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MALLLCFVLLCGVADLTRSLSTTPPEOMTEKAGETAYLPCRFLLGPEDEGPIIDIEMLLS 60
 DB 1 MALLLCFVLLCGVADPARSLSTTPPEMTEKAGETAYLPCRFLLSPEDGPIIDIEMLLS 60
 QY 61 PADNOKVDVYIILYSGDKIYDDYODLKGKRVHFTSNDLSKGASINVTNLQSLDICTYOC 120
 DB 61 PADNOKVDVYIILYSGDKIYDDYODLKGKRVHFTSNDLSKGASINVTNLQSLDICTYOC 120
 QY 121 KYKKAAGVGNKKIQLTVLLKPSGTRCYVDSSEIIGDFKICEPKKGSJPLQYEWOKLSD 180
 DB 121 KYKKAAGVGNKKIHLVLLVPSGARCYVDSSEIIGDFKICEPKKGSJPLQYEWOKLSD 180
 QY 181 SQKLPMTLAEEMTSPIVSVKNASTESYSGTCTVKRVGSDOCLRLDVPVPSNRAGTIA 240
 DB 181 SQKMPSTWLAEMTSVIVSVKNASSEYSGTCTVRRVSGDOCLRLNVPVPSNKAAGSSG 240
 QY 241 GA 242
 DB 241 GS 242
 RESULT 15
 AAW82731
 ID AAW82731 standard; Protein; 397 AA.
 XX
 AC AAW82731;
 XX
 DT 29-MAR-1999 (first entry)
 XX Adenovirus PACSG2SCAR.sig chimeric protein.

XX
 XX PACSG2SCAR.sigDEL; chimeric protein; adenoviral fibre protein;
 KW trimerisation domain; affinity; substrate; gene therapy vector;
 KW infection; attachment; interaction assay; vector; monomer.
 XX
 OS Mastadenovirus.
 OS Synthetic.
 XX WO9854346-A1.
 XX
 PD 03-DEC-1998.
 XX
 PF 28-MAY-1998; 98WO-US11024.
 XX
 PR 16-JAN-1998; 98US-0071668.
 PR 28-MAY-1997; 97US-0047849.
 XX
 PA (GENV-) GENVEC INC.
 XX
 PI Brough DE, Einfield D, Kovesdi I, Lizonova A, Roelvink PW;
 PI Wickham TJ, Yonehiro G;
 XX
 DR WPI: 1999-059848/05.
 DR N-PSDB; AAV72027.
 XX
 PT New adenoviral fibre trimer with reduced binding to native substrate
 PT - useful for, e.g. preparing gene therapy vector with minimal
 PT ectopic infection for in vitro applications
 XX
 PS Example 10; Page 60-62; 103pp; English.
 XX
 CC This sequence represents a novel adenovirus chimeric protein,
 CC PACSG2SCAR.sigDEL. This protein is used in a method for the
 CC construction of novel monomers having an N-terminus of an adenoviral
 CC fibre protein and a trimerisation domain. Such monomers have lower
 CC affinity for native substrate than the native adenoviral fibre trimer.
 CC Cell lines containing such monomers are used (i) to propagate adenovirus
 CC for use as gene therapy vectors (for in vitro or in vivo applications,
 CC (ii) as reagents for studying adenoviral attachment and infection, and
 CC (iii) in receptor-ligand interaction assays. The new viruses produce
 CC minimal ectopic infection (they can not infect native host cells) so are
 CC safer as vectors and can be engineered for selective targeting to other
 CC cells.
 XX
 SQ Sequence 397 AA;
 Query Match 84.0%; Score 1142; DB 20; Length 397;
 Best Local Similarity 88.4%; Pred. No. 3.4e-99;
 Matches 214; Conservative 15; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MALLLCFVLLCGVADLTRSLSTTPPEOMTEKAGETAYLPCRFLLGPEDEGPIIDIEMLLS 60
 DB 1 MALLLCFVLLCGVADPARSLSTTPPEMTEKAGETAYLPCRFLLSPEDGPIIDIEMLLS 60
 QY 61 PADNOKVDVYIILYSGDKIYDDYODLKGKRVHFTSNDLSKGASINVTNLQSLDICTYOC 120
 DB 61 PADNOKVDVYIILYSGDKIYDDYODLKGKRVHFTSNDLSKGASINVTNLQSLDICTYOC 120
 QY 121 KYKKAAGVGNKKIQLTVLLKPSGTRCYVDSSEIIGDFKICEPKKGSJPLQYEWOKLSD 180
 DB 121 KYKKAAGVGNKKIHLVLLVPSGARCYVDSSEIIGDFKICEPKKGSJPLQYEWOKLSD 180
 QY 181 SQKLPMTLAEEMTSPIVSVKNASTESYSGTCTVKRVGSDOCLRLDVPVPSNRAGTIA 240
 DB 181 SQKMPSTWLAEMTSVIVSVKNASSEYSGTCTVRRVSGDOCLRLNVPVPSNKAAGSSG 240
 QY 241 GA 242
 DB 241 GS 242
 Search completed: July 9, 2003, 12:44:32
 Job time : 38 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 12:43:53 ; Search time 14 Seconds
(without alignments)
548.527 Million cell updates/sec

Title: US-09-899-634C-2

Perfect score: 1359
Sequence: 1 MALLICFVLICGVADLTSL.....AVIGVLLALVILGIFCCR 261Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCITUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	91.1	365	2	US-08-979-424-3
2	1238	91.1	365	4	US-09-272-496-2
3	1224	90.1	365	4	US-08-928-3838-2
4	1217	89.6	365	4	US-08-928-3838-23
5	1217	89.6	365	4	US-08-928-3838-23
6	1216	89.5	365	4	US-08-928-3838-26
7	523	38.5	106	4	US-08-928-3838-8
8	453	33.3	95	4	US-08-928-3838-17
9	351.5	25.9	273	4	US-09-254-465A-26
10	351.5	25.9	319	1	US-08-597-495B-22
11	351.5	25.9	319	4	US-09-068-051A-22
12	351.5	25.9	319	4	US-09-336-536-67
13	351.5	25.9	319	4	US-09-254-465A-6
14	341.5	23.2	270	4	US-09-254-465A-32
15	315.5	23.1	318	4	US-09-068-051A-32
16	258	19.0	387	4	US-09-175-928-2
17	246.5	18.1	394	4	US-09-336-536-39
18	244	18.0	365	4	US-09-336-536-40
19	217	16.0	380	2	US-08-979-424-1
20	199.5	14.7	249	4	US-09-336-536-42
21	196	14.4	299	4	US-09-188-930-331
22	196	14.4	299	4	US-09-462-270-2
23	196	14.4	299	4	US-09-254-465A-1
24	191	14.1	299	4	US-09-188-930-189
25	190	14.0	370	4	US-09-336-536-28
26	189	13.9	341	4	US-09-336-536-29
27	184	13.5	263	4	US-09-254-465A-25

28	181.5	13.4	312	4	US-09-254-465A-9	Sequence 9, App1
29	180	13.2	260	4	US-09-254-465A-23	Sequence 23, App1
30	178.5	13.1	298	4	US-09-152-060-76	Sequence 76, App1
31	163.5	12.0	321	4	US-09-254-465A-2	Sequence 2, App1
32	163	12.0	246	4	US-09-336-536-31	Sequence 31, App1
33	161.5	11.9	300	4	US-09-254-465A-10	Sequence 10, App1
34	158	11.6	209	4	US-09-430-503-20	Sequence 20, App1
35	158	11.6	209	4	US-09-430-503-24	Sequence 24, App1
36	156	11.5	209	4	US-09-430-503-18	Sequence 18, App1
37	156	11.5	209	4	US-09-430-503-22	Sequence 22, App1
38	155	11.4	269	4	US-09-430-503-4	Sequence 4, App1
39	155	11.4	269	4	US-09-430-503-6	Sequence 6, App1
40	155	11.4	269	4	US-09-430-503-8	Sequence 8, App1
41	154	11.3	306	4	US-08-205-697A-17	Sequence 17, App1
42	154	11.3	306	4	US-08-702-525-17	Sequence 17, App1
43	154	11.3	306	4	US-09-651-200-17	Sequence 17, App1
44	154	11.3	306	5	PCT-US95-02576-17	Sequence 17, App1
45	153	11.3	269	4	US-09-430-503-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-08-979-424-3
; Sequence 3, Application US/08979424
; Patent No. 5942606
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/979,424
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0405 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1946351
; US-08-979-424-3
Query Match 91.1%; Score 1238; DB 2; Length 365;
Best Local Similarity 89.3%; Pred. No. 16-114;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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QY      1 MALLLCFVLLCGVADLTRSLSTTPEOMIEKAGETAYLPCRFLLGPEDDGPIIDIEWLIS 60
      1 MALLLCFVLLCGVADLTRSLSTTPEOMIEKAGETAYLPCRFLLGPEDDGPIIDIEWLIS 60
Db      1 MALLLCFVLLCGVADLTRSLSTTPEOMIEKAGETAYLPCRFLLGPEDDGPIIDIEWLIS 60
QY      61 PADNOKVQDVYIILYSGDKIYDDYODLKGKRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
      61 PADNOKVQDVYIILYSGDKIYDDYODLKGKRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
Db      61 PADNOKVQDVYIILYSGDKIYDDYODLKGKRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
QY      121 KYKKAAGVGNKKIQLTVLKPSTRCYVDGSEIIGNDPKLCEPKEGSLPLYEMOKLSN 180
      121 KYKKAAGVGNKKIQLTVLKPSTRCYVDGSEIIGNDPKLCEPKEGSLPLYEMOKLSN 180
Db      121 KYKKAAGVGNKKIQLTVLKPSTRCYVDGSEIIGNDPKLCEPKEGSLPLYEMOKLSN 180
QY      181 SQKPLPTLWLAEMTSPIVSKNASTEYSGTYSCTVKRNVGSDQCLRLDVVPPSNRAGTIA 240
      181 SQKPLPTLWLAEMTSPIVSKNASTEYSGTYSCTVKRNVGSDQCLRLDVVPPSNRAGTIA 240
Db      181 SQKPLPTLWLAEMTSPIVSKNASTEYSGTYSCTVKRNVGSDQCLRLDVVPPSNRAGTIA 240
QY      241 GAVIGVLALVLIIGLIIFCCR 261
      241 GAVIGVLALVLIIGLIIFCCR 261
Db      241 GAVIGVLALVLIIGLIIFCCR 261

```

RESULT 2

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US-09-272-496-2
; Sequence 2, Application US/09272496
; Patent No. 6245966
; GENERAL INFORMATION:
; APPLICANT: Degregori, James
; TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
; FILE REFERENCE: 90-98
; CURRENT APPLICATION NUMBER: US/09/272.496
; CURRENT FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: US 60/092782
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-272-496-2

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Query Match      91.1%; Score 1238; DB 4; Length 365;
Best Local Similarity 89.3%; Pred. NO. 1e-114;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY      1 MALLLCFVLLCGVADLTRSLSTTPEOMIEKAGETAYLPCRFLLGPEDDGPIIDIEWLIS 60
      1 MALLLCFVLLCGVADLTRSLSTTPEOMIEKAGETAYLPCRFLLGPEDDGPIIDIEWLIS 60
Db      1 MALLLCFVLLCGVADLTRSLSTTPEOMIEKAGETAYLPCRFLLGPEDDGPIIDIEWLIS 60
QY      61 PADNOKVQDVYIILYSGDKIYDDYODLKGKRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
      61 PADNOKVQDVYIILYSGDKIYDDYODLKGKRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
Db      61 PADNOKVQDVYIILYSGDKIYDDYODLKGKRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
QY      121 KYKKAAGVGNKKIQLTVLKPSTRCYVDGSEIIGNDPKLCEPKEGSLPLYEMOKLSN 180
      121 KYKKAAGVGNKKIQLTVLKPSTRCYVDGSEIIGNDPKLCEPKEGSLPLYEMOKLSN 180
Db      121 KYKKAAGVGNKKIQLTVLKPSTRCYVDGSEIIGNDPKLCEPKEGSLPLYEMOKLSN 180
QY      181 SQKPLPTLWLAEMTSPIVSKNASTEYSGTYSCTVKRNVGSDQCLRLDVVPPSNRAGTIA 240
      181 SQKPLPTLWLAEMTSPIVSKNASTEYSGTYSCTVKRNVGSDQCLRLDVVPPSNRAGTIA 240
Db      181 SQKPLPTLWLAEMTSPIVSKNASTEYSGTYSCTVKRNVGSDQCLRLDVVPPSNRAGTIA 240
QY      241 GAVIGVLALVLIIGLIIFCCR 261
      241 GAVIGVLALVLIIGLIIFCCR 261
Db      241 GAVIGVLALVLIIGLIIFCCR 261

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RESULT 3

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US-08-928-383B-2
; Sequence 2, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
;

```

```

; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921e1 Coxsackievirus and Adenovirus
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-928-383B-2

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Query Match      90.1%; Score 1224; DB 4; Length 365;
Best Local Similarity 88.9%; Pred. No. 2.5e-113;
Matches 232; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY      1 MALLLCFVLLCGVADLTRSLSTTPEOMIEKAGETAYLPCRFLLGPEDDGPIIDIEWLIS 60
      1 MALLLCFVLLCGVADLTRSLSTTPEOMIEKAGETAYLPCRFLLGPEDDGPIIDIEWLIS 60
Db      1 MALLLCFVLLCGVADLTRSLSTTPEOMIEKAGETAYLPCRFLLGPEDDGPIIDIEWLIS 60
QY      61 PADNOKVQDVYIILYSGDKIYDDYODLKGKRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
      61 PADNOKVQDVYIILYSGDKIYDDYODLKGKRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
Db      61 PADNOKVQDVYIILYSGDKIYDDYODLKGKRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
QY      121 KYKKAAGVGNKKIQLTVLKPSTRCYVDGSEIIGNDPKLCEPKEGSLPLYEMOKLSN 180
      121 KYKKAAGVGNKKIQLTVLKPSTRCYVDGSEIIGNDPKLCEPKEGSLPLYEMOKLSN 180
Db      121 KYKKAAGVGNKKIQLTVLKPSTRCYVDGSEIIGNDPKLCEPKEGSLPLYEMOKLSN 180
QY      181 SQKPLPTLWLAEMTSPIVSKNASTEYSGTYSCTVKRNVGSDQCLRLDVVPPSNRAGTIA 240
      181 SQKPLPTLWLAEMTSPIVSKNASTEYSGTYSCTVKRNVGSDQCLRLDVVPPSNRAGTIA 240
Db      181 SQKPLPTLWLAEMTSPIVSKNASTEYSGTYSCTVKRNVGSDQCLRLDVVPPSNRAGTIA 240
QY      241 GAVIGVLALVLIIGLIIFCCR 261
      241 GAVIGVLALVLIIGLIIFCCR 261
Db      241 GAVIGVLALVLIIGLIIFCCR 261

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RESULT 4

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US-08-928-383B-23
; Sequence 23, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; TITLE OF INVENTION: CAR, A No. 6210921e1 Coxsackievirus and Adenovirus
; NUMBER OF SEQUENCES: 26

```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD, LLP
;; STREET: 28 State Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/928,383B
;; FILING DATE: 12-SEP-1997
;;
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/026,100
;; FILING DATE: 13-SEP-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mandragouras, Amy E.
;; REGISTRATION NUMBER: 36,207
;; REFERENCE/DOCKET NUMBER: DFN-020
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)742-4214
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 365 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal
;;
;; US-08-928-383B-23

Query Match 89.6%; Score 1217; DB 4; Length 365;
Best Local Similarity 88.1%; Pred. No. 1.2e-112;
Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTSLSTITPEOMTEKAGETAYLPCEFTLGPEDQGLDIEWLIS 60
DB 1 MARLLCFVLLCGIADLTSLSTITPEORIEKAGETAYLPCKFTLSPEDEQGLDIEWLIS 60
QY 61 PADNOKVQDVIILYSGDKTYDDYODLKGKRVHFTSNDLKSAGASINVTMLQSLDICTYOC 120
DB 61 PSNNOIVDQVILYSGDKTYDDYODLKGKRVHFTSNDVSGASINVTMLQSLDICTYOC 120
QY 121 KYKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFLKEPKEGSLPLLEYMOKLSN 180
DB 121 KYKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFLKEPKEGSLPLLEYMOKLSN 180
QY 181 SOKLPTLMLAEMTSPIVSKNASTEYSGTYSCTVKNRVGSDOCLRLDVPVPSNRAGTIA 240
DB 181 SOKLPTLMLAEMTSPIVSKNASTEYSGTYSCTVKNRVGSDOCLRLDVPVPSNRAGTIA 240
QY 241 GAVIGVLLALVLIGLIIFCC 260
DB 241 GAVIGVLLALVLIGLIIFCC 260

RESULT 5
US-08-928-383B-24
; Sequence 24, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Cocksackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/928,383B
;; FILING DATE: 12-SEP-1997
;;
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/026,100
;; FILING DATE: 13-SEP-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mandragouras, Amy E.
;; REGISTRATION NUMBER: 36,207
;; REFERENCE/DOCKET NUMBER: DFN-020
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)742-4214
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 365 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal
;;
;; US-08-928-383B-24

Query Match 89.6%; Score 1217; DB 4; Length 365;
Best Local Similarity 88.1%; Pred. No. 1.2e-112;
Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTSLSTITPEOMTEKAGETAYLPCEFTLGPEDQGLDIEWLIS 60
DB 1 MARLLCFVLLCGIADLTSLSTITPEORIEKAGETAYLPCKFTLSPEDEQGLDIEWLIS 60
QY 61 PADNOKVQDVIILYSGDKTYDDYODLKGKRVHFTSNDLKSAGASINVTMLQSLDICTYOC 120
DB 61 PSNNOIVDQVILYSGDKTYDDYODLKGKRVHFTSNDVSGASINVTMLQSLDICTYOC 120
QY 121 KYKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFLKEPKEGSLPLLEYMOKLSN 180
DB 121 KYKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFLKEPKEGSLPLLEYMOKLSN 180
QY 181 SOKLPTLMLAEMTSPIVSKNASTEYSGTYSCTVKNRVGSDOCLRLDVPVPSNRAGTIA 240
DB 181 SOKLPTLMLAEMTSPIVSKNASTEYSGTYSCTVKNRVGSDOCLRLDVPVPSNRAGTIA 240
QY 241 GAVIGVLLALVLIGLIIFCC 260
DB 241 GAVIGVLLALVLIGLIIFCC 260

RESULT 6
US-08-928-383B-26
; Sequence 26, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Cocksackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-928-383B-26

Query Match 89.5%; Score 1216; DB 4; Length 365;
Best Local Similarity 88.1%; Pred. No. 1.6e-112;
Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MALLTGVLLCGVADLTRSLITTPPEQMEKAGETAYLPCRFLLGPEDEGPDIDIELLS 60
DB 1 MALLTGVLLCGVADLTRSLITTPPEQMEKAGETAYLPCRFLLGPEDEGPDIDIELLS 60
QY 61 PADNQRVDQYIILYSGDKIYDDYQDLKGRVHTSNDLKSQDASINVTNLQSLDIGTYQC 120
DB 61 PSBNOIVDQYIILYSGDKIYDDYQDLKGRVHTSNDLKSQDASINVTNLQSLDIGTYQC 120
QY 121 KYKAGVGNKKIQLTVLKPSTRCVDSSEIINDFKLCKPKKESLPLQFEMQKLS 180
DB 121 KYKAGVGNKKIQLTVLKPSTRCVDSSEIINDFKLCKPKKESLPLQFEMQKLS 180
QY 181 SQKPLTLMIAEMTSPVIVSNASTEXSGTCTVKNRVGSDQCLRLDVPVPSNRAQTIA 240
DB 181 SQKPLTLMIAEMTSPVIVSNASTEXSGTCTVKNRVGSDQCLRLDVPVPSNRAQTIA 240
QY 241 GAVIGVLLALVILGLIFCC 260
DB 241 GAVIGVLLALVILGLIFCC 260

RESULT 7
US-08-928-383B-8
Sequence 8, Application US/08928383B
Patent No. 6210921
GENERAL INFORMATION:
APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
APPLICANT: and Marshall S. Horwitz
TITLE OF INVENTION: CAR, A No. 6210921el Coxsackievirus and Adenovirus
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-928-383B-8

Query Match 38.5%; Score 523; DB 4; Length 106;
Best Local Similarity 92.5%; Pred. No. 1.4e-44;
Matches 98; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 34 GETAYLPCRFLLGPEDEGPDIDIELLSPADNQRVDQYIILYSGDKIYDDYQDLKGRVHF 93
DB 1 GETAYLPCRFLLGPEDEGPDIDIELLSPADNQRVDQYIILYSGDKIYDDYQDLKGRVHF 93
QY 94 TSNDLKSQDASINVTNLQSLDIGTYQCKVKKAPGVGNKKIQLTVLL 139
DB 61 TSNDLKSQDASINVTNLQSLDIGTYQCKVKKAPGVGNKKIQLTVLL 139

RESULT 8
US-08-928-383B-17
Sequence 17, Application US/08928383B
Patent No. 6210921
GENERAL INFORMATION:
APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
APPLICANT: and Marshall S. Horwitz
TITLE OF INVENTION: CAR, A No. 6210921el Coxsackievirus and Adenovirus
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400

Qy	240	AGAVIGVLLALVLIIGLIIFCC	260
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Db	239	VGIAVGVAALIIIGIIYYCC	259

RESULT 11
HS-09-068

US-09-068-051A-22
Sequence 22, Application US/09068051A
Patent No. 6291235
GENERAL INFORMATION:
APPLICANT: Old, Lloyd J.; Well, Sydney; Rittner, Gerd;
Samson, Richard J.; Nice, Edouard; Moritz,
Caimen, B.; Ji, Hong; Burgess, Anthony W.;
Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,051A
FILING DATE: 10-Dec-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597,495
FILING DATE: 02-Feb-1996
APPLICATION NUMBER: 08/511,876
FILING DATE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6291235man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5316.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 22
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 22
US-09-068-051A-22

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QY      240 AGAVIGVLLALVLIGLIIFCC 260
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Db      239 VGIAVGVALIIGIITYCC 259
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RESULT 12
IIS-09-336

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US-09-336-536-67
Sequence 67, Application US/09336536
Patent No. 6406884
GENERAL INFORMATION
APPLICANT: leihey, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336, 536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 67
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-09-336-536-67

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RESULT 13

US-09-254-465A-6
Sequence 6, Application US/09254465A
Patent No. 6410708
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Napier, Mary A.
APPLICANT: Tuma, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
OF INFECTIONS OF DISORDERS CHARACTERIZED BY A3- RELATED ANTIGENS
FILE REFERENCE: P1216R(US)
CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: PCT/US98/24855
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: US 60/066,364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 60/078,936

[illegible]

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Db      7 A1SVEITPDVLAAGQGSVTLPCYTHYSTSSREGI-IQMDKULLT-----HIERVYIMPF 60
OY      76 GDK--YDDYQDLKGRVHTSNLDKSGDASINVTNLQSDIGYQCKYKAPGV-GNKK 132
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 SNKVYIHGELY---KNRVSI-SNNAGSDASITIDQLTMADNGTYECGVSILMSDEGNKT 116
OY      133 --IQLTVLKSGRCYVDGSEETIGNDPKLCEPREGSLPLIYEQKLS-NSQKPLTML 189
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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OY      190 AEMTS-PIASVKNASTEVSGTSCYTKVRVGSDOCLRLRDVYPPSNRAGTIGAVYGVLL 248
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
        174 AQPASGQVSLAKNISTDPSGYIITCTSSNEBGTFCNITVAVRSPSNVYALYGIAGVVA 233
Db      249 ALVLIIGLIIFCC 260
OY      234 ALIIGLIITCC 245
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RESULT 15
US-09-068-051A-32
; Sequence 32, Application US/09068051A
; Patent No. 6291235
GENERAL INFORMATION:
APPLICANT: Old, Lloyd J.; Wolt, Sydney; Ritter, Gerd;
Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
Cathel, B.; Ji, Hong; Burgess, Anthony W.;
Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068, 051A
FILING DATE: 10-Dec-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597,495
FILING DATE: 02-Feb-1996
APPLICATION NUMBER: 08/511,876
FILING DATE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson; No. 6291235man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5316.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 32
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32
US-09-068-051A-32
Query Match      23.2%; Score 315.5; DB 4; Length 318;
Best Local Similarity 30.7%; Pred. No. 2.7e-23;
Matches      81; Conservative 50; Mismatches 106; Indels 27; Gaps 10;
9  LLGCVADITRSLSTTPEQMIKAKGFAVYPCRFLLPEDQGPLDIEM--LLSPADNQK 66

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 12:44:38 ; Search time 23 Seconds

(without alignments)
1321.111 Million cell updates/sec

Title: US-09-899-634C-2

Perfect score: 1359
Sequence: 1 MALLLCEVLLCGVADITRSL.....AVIGVLLALVILGILIFCCR 261

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Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
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2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/PCT05_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
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14: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1359	100.0	261	10 US-09-899-634A-2	Sequence 2, Appl
2	1353	99.6	365	10 US-09-899-634A-4	Sequence 4, Appl
3	1238	91.1	352	9 US-09-992-598-505	Sequence 505, App
4	1238	91.1	352	9 US-09-989-293A-505	Sequence 505, App
5	1238	91.1	352	9 US-09-989-735-505	Sequence 505, App
6	1238	91.1	352	9 US-09-990-444-505	Sequence 505, App
7	1238	91.1	352	9 US-10-053-107-10	Sequence 10, Appl
8	1238	91.1	352	9 US-09-989-730-505	Sequence 505, App
9	1238	91.1	352	9 US-09-990-436-505	Sequence 505, App
10	1238	91.1	352	9 US-09-991-181-505	Sequence 505, App
11	1238	91.1	352	9 US-09-993-687-505	Sequence 505, App
12	1238	91.1	352	9 US-09-989-734-505	Sequence 505, App
13	1238	91.1	352	9 US-09-997-653-505	Sequence 505, App
14	1238	91.1	352	9 US-09-993-667-505	Sequence 505, App
15	1238	91.1	352	9 US-09-990-438-505	Sequence 505, App
16	1238	91.1	352	9 US-09-990-562-505	Sequence 505, App
17	1238	91.1	352	9 US-09-997-428-505	Sequence 505, App
18	1238	91.1	352	9 US-09-997-666-505	Sequence 505, App
19	1238	91.1	352	9 US-10-227-884-216	Sequence 216, App

20	1238	91.1	352	9 US-09-990-711-505	Sequence 505, App
21	1238	91.1	352	9 US-10-230-163-216	Sequence 216, App
22	1238	91.1	352	9 US-09-989-726-505	Sequence 505, App
23	1238	91.1	352	9 US-09-990-437-505	Sequence 505, App
24	1238	91.1	352	9 US-09-998-156-505	Sequence 505, App
25	1238	91.1	352	9 US-10-218-631-216	Sequence 216, App
26	1238	91.1	352	9 US-10-230-338-216	Sequence 216, App
27	1238	91.1	352	9 US-09-991-157-505	Sequence 505, App
28	1238	91.1	352	9 US-09-991-172-505	Sequence 505, App
29	1238	91.1	352	9 US-09-997-514-505	Sequence 505, App
30	1238	91.1	352	9 US-09-997-573-505	Sequence 505, App
31	1238	91.1	352	9 US-10-230-414-216	Sequence 216, App
32	1238	91.1	352	9 US-09-990-443-505	Sequence 505, App
33	1238	91.1	352	9 US-09-990-726-505	Sequence 505, App
34	1238	91.1	352	9 US-09-997-559-505	Sequence 505, App
35	1238	91.1	352	9 US-09-997-601-505	Sequence 505, App
36	1238	91.1	352	9 US-09-989-729A-505	Sequence 505, App
37	1238	91.1	352	9 US-09-990-440-505	Sequence 505, App
38	1238	91.1	352	9 US-09-991-854-505	Sequence 505, App
39	1238	91.1	352	9 US-09-997-349-505	Sequence 505, App
40	1238	91.1	352	9 US-09-997-440-505	Sequence 505, App
41	1238	91.1	352	9 US-09-997-628-505	Sequence 505, App
42	1238	91.1	352	9 US-09-997-683-505	Sequence 505, App
43	1238	91.1	352	9 US-10-213-145-10	Sequence 10, Appl
44	1238	91.1	352	9 US-09-993-463-505	Sequence 505, App
45	1238	91.1	352	9 US-09-993-748-505	Sequence 505, App

ALIGNMENTS

RESULT 1
US-09-899-634A-2
; Sequence 2, Application US/0989634A
; Patent No. US2002059654A1
; GENERAL INFORMATION:
; APPLICANT: Thomas Buehler, Reto Andreas Gadiant, Reinhard Korn, Rao Movva
; TITLE OF INVENTION: PCAR and its uses
; FILE REFERENCE: 4-31499A
; CURRENT APPLICATION NUMBER: US/09/899, 634A
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 261
; TYPE: PRT
; ORGANISM: porcine
US-09-899-634A-2

Query Match 100.0%; Score 1359; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 4.5e-89;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MALLLCEVLLCGVADITRSLSTITPPEOMIEKAKGETAYVPCFPTGPEDOGLDIEWLIS	60
DB	1	MALLLCEVLLCGVADITRSLSTITPPEOMIEKAKGETAYVPCFPTGPEDOGLDIEWLIS	60
QY	61	PADNOKVDPVITLLVSGDKYDIDYODLKGKRVFTSNDLSKGPASINVTNLQSDIGTYOC	120
DB	61	PADNOKVDPVITLLVSGDKYDIDYODLKGKRVFTSNDLSKGPASINVTNLQSDIGTYOC	120
QY	121	KYKKAAGVGNKKIQITVLLKPSGTRCYVDGSEIIGNDFLAKCEPREGSLPLLEYMOQLSN	180
DB	121	KYKKAAGVGNKKIQITVLLKPSGTRCYVDGSEIIGNDFLAKCEPREGSLPLLEYMOQLSN	180
QY	181	SKQLPTLWLAEMTSPVIVKNASTEXSGTCTVKNRVSGDOCLRLDVPVPSNRAGTIA	240
DB	181	SKQLPTLWLAEMTSPVIVKNASTEXSGTCTVKNRVSGDOCLRLDVPVPSNRAGTIA	240
QY	241	GAVIGVLLALVILGILIFCCR 261	
DB	241	GAVIGVLLALVILGILIFCCR 261	

RESULT 2
US-09-899-634A-4
; Sequence 4, Application US/09899634A
; Patent No. US20020059654A1
; GENERAL INFORMATION:
; APPLICANT: Thomas Buehler, Reto Andreas Gadiant, Reinhard Korn, Rao Movva
; TITLE OF INVENTION: pCAR and its uses
; FILE REFERENCE: 4-31499A
; CURRENT APPLICATION NUMBER: US/09/899,634A
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 365
; TYPE: PRT
; ORGANISM: porcine
US-09-899-634A-4

Query Match 99.6%; Score 1353; DB 10; Length 365;
Best Local Similarity 99.6%; Pred. No. 1,7e-88;
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALLCFVLLCGVADLTRSLSTTPPEOMIEKAGETAYLPQRFLLGPEDDGPDIDIEWLLS 60
DB 1 MALLCFVLLCGVADLTRSLSTTPPEOMIEKAGETAYLPQRFLLGPEDDGPDIDIEWLLS 60
QY 61 PADNOKVDQVYIIYSGDKIYDDYQDLKGRVHFTSNDLKSQDASINVTNLQSLDIGTYQC 120
DB 61 PADNOKVDQVYIIYSGDKIYDDYQDLKGRVHFTSNDLKSQDASINVTNLQSLDIGTYQC 120
QY 121 KVKKAPGVGNKKIQLTVLKPSGTRCYVDSSEIIGNDFKLKCEPKESLPLYLEWQKLSN 180
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QY 181 SOKLPTLMAMTSPTVSXKNASTEGTYSCTYKXRVGSDQCLRLDVPSPNRAGTIA 240
DB 181 SOKLPTLMAMTSPTVSXKNASTEGTYSCTYKXRVGSDQCLRLDVPSPNRAGTIA 240
QY 241 GAVIGVLLALVLLGLIIFCC 260
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RESULT 3
US-09-992-598-505
; Sequence 505, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC20
;; CURRENT APPLICATION NUMBER: US/09/992,598
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2,3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MALLLCFVLLCGVALLTSLSITTPQOMIEKAGETAVLPCRFETGPEPDGPILEWLLS 60
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Qy 121 KYKKAPEGVGNKKIQLTVLIKPSGTRCYVDGSEIINDFKLKEPEGSLPLLYEWOXLSN 180
Db 121 KYKKAPEGVGNKKIHVLVVKSGARCYVDGSEIISDPKIKCEPEGSLPLLYEWOXKSD 180
Qy 181 SOKLPTWLAEMTSVIVSKNASTESGYSCTVKNRVSDDCLRLNDVPPSNRAGTIA 240
Db 181 SOKMPTSWLAEMTSVIVSKNASTESGYSCTVKNRVSDDCLRLNDVPPSNRAGTIA 240
Qy 241 GAVIGVLLALVLIHIFCCR 261
Db 241 GAVIGVLLALVLIHIFCCR 261

RESULT 4
US-09-989-293A-505
; Sequence 505, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerdler, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2.3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLFVLLCGVADLTSLSTTPBOMTEKAGETAYLPCTTLGPEDOGPDIIMWLIS 60
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DB 181 SQKLPFLMLAEMTSPIVSVKNASTESGTYSCVTKORVSGDCLRLDVDVPPSNRAGTIA 240
QY 241 GAVIGVLLALVGLIIFCCR 261
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RESULT 5
US-09-899-735-505
; Sequence 505, Application US/0989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone

;; APPLICANT: Fong, Sherman
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;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C61
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445

PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090557
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2.3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MLLLCFVLGCVADLTRELSITTPPEOMTEKAKGETAYLPCRFITGPEPDGFLDIEMLS 60
DB 1 MLLLCFVLGCVADLTRELSITTPPEOMTEKAKGETAYLPCRFITGPEPDGFLDIEMLS 60
QY 61 PADNOKVDVILILYSGDKIYDDYODLKGKRVHFTSNDLSKGDASINVTNLQSLDICTYOC 120
DB 61 PADNOKVDVILILYSGDKIYDDYODLKGKRVHFTSNDLSKGDASINVTNLQSLDICTYOC 120
QY 121 KYKAPGVGNKKIQLTVLILKPSGTRCYVDGSEIEGDFLKEPPEKGSJPLLYEWOXLSN 180
DB 121 KYKAPGVGNKKIQLTVLILKPSGTRCYVDGSEIEGDFLKEPPEKGSJPLLYEWOXLSN 180
QY 181 SOKLPTMLAEMTSPVIVKRNASTYSGTCTVKNRVGSDOCLRLDVVPPSNRAGTIA 240
DB 181 SOKLPTMLAEMTSPVIVKRNASTYSGTCTVKNRVGSDOCLRLDVVPPSNRAGTIA 240
QY 241 GAVIGVLAIVLIGLIIFFCCR 261
DB 241 GAVIGVLAIVLIGLIIFFCCR 261

RESULT 6
US-09-990-444-505

Sequence 505, Application US/09990444
Publication No. US20020193300A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1c19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
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PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;

Best Local Similarity 89.3%; Pred. No. 2,3e-80; Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLICFVLLCGVADLTRSLITTPPEOMIKAKGETAYLPORFTLGEDEGPIIDIEWLLS 60
DB 1 MALLICFVLLCGVADLTRSLITTPPEOMIKAKGETAYLPORFTLGEDEGPIIDIEWLLS 60
QY 61 PANOQKDYVITILYSGKTYDDYQDLKGRVHFNSNLSKGDASINTNTQLSDIGTYOC 120
DB 61 PANOQKDYVITILYSGKTYDDYQDLKGRVHFNSNLSKGDASINTNTQLSDIGTYOC 120
QY 121 KVKKAPGVNKKIQLTFLKPSGTRCVYDGSSEITGNDFLXKCEPKESGLPLAYEMOKLSN 180
DB 121 KVKKAPGVNKKIHLVVLVPSGARCTVYDGSSEITGNDFLXKCEPKESGLPLAYEMOKLSN 180
QY 181 SOKLPTLMAEMTSVTSVKNASTSEYSGTYSCTVKNVSGDOCLRLDVPSPSNAQTIA 240
DB 181 SOKLPTLMAEMTSVTSVKNASTSEYSGTYSCTVKNVSGDOCLRLDVPSPSNAQTIA 240

DB 181 SOKMPTSLMAEMTSVTSVKNASTSEYSGTYSCTVKNVSGDOCLRLDVPSPSNAQTIA 240
QY 241 GAVIGVLALVLIIGLIIFCCR 261
DB 241 GAVIGVLALVLIIGLIIFCCR 261

RESULT 7
US-10-053-107-10
Sequence 10, Application US/10053107
Publication No. US20020192752A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
FILE OF INVENTION: Related Diseases
FILE REFERENCE: P3033R1C1
CURRENT APPLICATION NUMBER: US/10/053,107
PRIOR FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 60/099601
PRIOR FILING DATE: 19998-09-09
PRIOR APPLICATION NUMBER: 60/107783
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 60/108802
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
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PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/209832
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/218517
PRIOR FILING DATE: 1998-12-22
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PRIOR FILING DATE: 1999-01-05
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PRIOR FILING DATE: 1999-09-01
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PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: PCT/US00/15264
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PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
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PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 14

SEQ ID NO 10
LENGTH: 352
TYPE: PRT
ORGANISM: Homo Sapien
US-10-053-107-10

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2.3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLFEVLLCGVADLTRSITTPBOMTEKAGETAYLCRFTLIGEDDGLDIEMLLS 60
DB 1 MALLLFEVLLCGVADTPARSITTPBEMTEKAGETAYLCRFTLIGEDDGLDIEMLLS 60
QY 61 PADNOKVDQYIILYSGDKIYDYODLKGHVHTSNDLKSAGASINVTNLQSLDIGTYQC 120
DB 61 PADNOKVDQYIILYSGDKIYDYODLKGHVHTSNDLKSAGASINVTNLQSLDIGTYQC 120
QY 121 KVKKAGVGNKKIQLVYLKPSGTRCYVDGSEIINDFKLCEPKRGSLPLLYEWMKLSN 180
DB 121 KVKKAGVGNKKIHLVYLKPSGARCVDSSEIIGSPFKICEPKRGSLPLQYEWQKLSN 180
QY 181 SOKLPTLMLAEMTSPIYSVKNASTREYSGTSCVKNRVSGDCLLRLDVVPSPNRAGTIA 240
DB 181 SQMPTSLAEMTSVIVSVKNASSEYSGTSCVKNRVSGDCLLRLDVVPSPNRAGTIA 240
QY 241 GAVIGVLLALVLLGLIIFCCR 261
DB 241 GAVIGVLLALVLLGLIIFCCR 261

RESULT 8

US-09-989-730-505
Sequence 505, Application US/09989730

Publication No. US20020197674A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Nadjler, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC69
CURRENT APPLICATION NUMBER: US/09/989, 730
PRIOR APPLICATION NUMBER: 2001-11-20
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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PRIOR APPLICATION NUMBER: 60/087759
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PRIOR FILING DATE: 1998-06-04
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7 PRIOR FILING DATE: 1998-06-17
8 PRIOR APPLICATION NUMBER: 60/089600
9 PRIOR FILING DATE: 1998-06-17
10 PRIOR APPLICATION NUMBER: 60/089653
11 PRIOR FILING DATE: 1998-06-17
12 PRIOR APPLICATION NUMBER: 60/089801
13 PRIOR FILING DATE: 1998-06-18
14 PRIOR APPLICATION NUMBER: 60/089907
15 PRIOR FILING DATE: 1998-06-18
16 PRIOR APPLICATION NUMBER: 60/089908
17 PRIOR FILING DATE: 1998-06-18
18 PRIOR APPLICATION NUMBER: 60/089947
19 PRIOR FILING DATE: 1998-06-19
20 PRIOR APPLICATION NUMBER: 60/089948
21 PRIOR FILING DATE: 1998-06-19
22 PRIOR APPLICATION NUMBER: 60/089952
23 PRIOR FILING DATE: 1998-06-19
24 PRIOR APPLICATION NUMBER: 60/090246
25 PRIOR FILING DATE: 1998-06-22
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27 PRIOR FILING DATE: 1998-06-22
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36 PRIOR APPLICATION NUMBER: 60/090431
37 PRIOR FILING DATE: 1998-06-24
38 PRIOR APPLICATION NUMBER: 60/090435
39 PRIOR FILING DATE: 1998-06-24
40 PRIOR APPLICATION NUMBER: 60/090444
41 PRIOR FILING DATE: 1998-06-24
42 PRIOR APPLICATION NUMBER: 60/090445
43 PRIOR FILING DATE: 1998-06-24
44 PRIOR APPLICATION NUMBER: 60/090472
45 PRIOR FILING DATE: 1998-06-24
46 PRIOR APPLICATION NUMBER: 60/090535
47 PRIOR FILING DATE: 1998-06-24
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69 PRIOR FILING DATE: 1998-06-26
70 PRIOR APPLICATION NUMBER: 60/091360
71 PRIOR FILING DATE: 1998-07-01
72 PRIOR APPLICATION NUMBER: 60/091478
73 PRIOR FILING DATE: 1998-07-02

1 PRIOR APPLICATION NUMBER: 60/091544
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3 PRIOR APPLICATION NUMBER: 60/091519
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5 PRIOR APPLICATION NUMBER: 60/091626
6 PRIOR FILING DATE: 1998-07-02
7 PRIOR APPLICATION NUMBER: 60/091633
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9 PRIOR APPLICATION NUMBER: 60/091978
10 PRIOR FILING DATE: 1998-07-07
11 PRIOR APPLICATION NUMBER: 60/091982
12 PRIOR FILING DATE: 1998-07-07
13 PRIOR APPLICATION NUMBER: 60/092182
14 PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2, 3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTSLSTTTPEQMIKAKGETAYLPCRFYLGPEDDGPIIDIEWLLS 60
DB 1 MALLLCFVLLCGVADLTSLSTTTPEQMIKAKGETAYLPCRFYLGPEDDGPIIDIEWLLS 60
QY 61 PADNOKVDVYIILYSGDKYDDYODLKRVRHFTSNLKSQDASTNVTYLOLSDICTYQC 120
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QY 121 KYKAKGVGNKKIKQLVLLKPSGTRCYVDGSEIEGNDFKLCEPKESLPLLYEMOKLSN 180
DB 121 KYKAKGVGNKKIKHLVLLKPSGARCYVDGSEIEGDFIKCEPKESLPLLYEMOKLSD 180
QY 181 SQKPLTFLAEMTSPVISYKNASTEXSGTYSCTVKNRVSSDOCLRLDVPSPNKAQTIA 240
DB 181 SQKPLTFLAEMTSPVISYKNASTEXSGTYSCTVKNRVSSDOCLRLDVPSPNKAQTIA 240
QY 241 GAVTGVLLALVLIIGLIIFCCR 261
DB 241 GAVTGVLLALVLIIGLIIFCCR 261

RESULT 9
US-09-990-436-505
Sequence 505, Application US/09990436
Publication No. US20020198148A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436

1	CURRENT FILING DATE: 2001-11-14
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72	PRIOR FILING DATE: 1998-06-25
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09
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Query Match      91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2.3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
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DB 1 MALLCFVLLCGVADLTSLSTTPPEQMIKAGETRYLFCRFTLGEDEGPDIDIEWLLS 60
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DB 61 PADNOKVDQYIIYSGDKIYDYQDLKGRVHFTSNDLKSQDASINTVNLQSLDIGTYQC 120
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DB 121 KVKKAPGVNKKIQLTVLLKPSGTCYVDGSEETIGNDFKLCPEKESGSLPLYEWOKLSN 180
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QY 181 SQTLPITLMAEMTSVSVNASTVEYSGTSCVTKRVGSDQCLRLDVVPPNRACTIA 240
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RESULT 10

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; Sequence 505, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guirney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napiet, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC53
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1997-10-17
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred No. 2.3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTBSLSTTPEOMIEKAGETAYLPCRFLLGPEDQGLDIEMWLS 60
DB 1 MALLLCFVLLCGVDFARSLSTTPEEMIEKAGETAYLPCRFLLSPEDQGLDIEMWLS 60
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QY 181 SOKLPTLMLAEMTSFVIVKNASTEYSCTGVKRVGSDOCLRLDVPPSNAGTIA 240
DB 181 SOKMPTSWLAEMTSFVIVKNASTEYSCTGVKRVGSDOCLRLDVPPSNAGTIA 240
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DB 241 GAVIGVLLALVILGLIIFCCR 261

RESULT 11
US-09-993-687-505
; Sequence 505, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2.3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLFVLLCGVADLTSLSTTPPOMIEKAGETAYLPFCRTTLGPEDOGPIIDIMELIS 60
DB 1 MALLLFVLLCGVADLTSLSTTPPOMIEKAGETAYLPFCRTTLGPEDOGPIIDIMELIS 60
QY 61 PADNOKVDOYIIYSGDKIYDDYYODLKGHVHFTSNDLKSQDASINVTNLQSLDIGYOC 120
DB 61 PADNOKVDOYIIYSGDKIYDDYYODLKGHVHFTSNDLKSQDASINVTNLQSLDIGYOC 120
QY 121 KYKKAQGVGNKKIQLTVLLKPSGTRCVDSSEIIGNDFLKKCEPKSGSJPLYEMOKLSN 180
DB 121 KYKKAQGVGNKKIQLTVLLKPSGTRCVDSSEIIGNDFLKKCEPKSGSJPLYEMOKLSN 180
QY 181 SQKLPFLMLAEMTSPIYSVNASTETYSCTYKAKRVSGDQCLRLDVPSPNRAGTTA 240
DB 181 SQKLPFLMLAEMTSPIYSVNASTETYSCTYKAKRVSGDQCLRLDVPSPNRAGTTA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 12
US-09-989-734-505
; Sequence 505, Application US/09989734
; Publication No. US20030003531A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.

;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Geritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tuma, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C64
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/0921822
PRIOR FILING DATE: 1998-07-09

Query Match	91.1%	Score 1238;	DB 9;	Length 352;
Best Local Similarity	89.3%	Pred. No. 2.3e-80;		
Matches 233; Conservative	13;	Mismatches 15;	Indels. 0;	Gaps 0;

Qy	1	MALLFEVLLCGVAALITLSLSITTEPEQMI EKAKETALPRFLIGDEGQPLDIEMLLS	60
Db	1	MALLFEVLLCGVADVPARSISITTEPEEMI EKAKETALPRCKFLTSPEDQPLDIEMLLS	60
Qy	61	PADNOKVDOVITLLYSGDKIYDDYVODLGRHVFHSNDLKSDBASINVTNIOLSIGYOC	120
Db	61	PANQVADVIVITLLYSGDKIYDDYVYDVLGRHVFHSNDLKSDBASINVTNIOLSIGYOC	120
Qy	121	KVKKABGVGNKKIOITVLLKPSGTCYVDGSEETIGNDPFKLKCEPEKGSPLLYEWMQLSN	180
Db	121	KVKKAGVGNKKIHHIVLTKPSGAPCYVDGSEETIGSPFKIKCEPEKESPLQIYEWQMLSD	180
Qy	181	SOKLPLTLAEMTSPVIVSKNASTEGTGYCTYKNRGSQDCLRLDYVPSPNRBACTIA	240
Db	181	SQKMPFSMLAEMTSSVIVSKNASTSYGTYCTYRNRVGSQDCLRLRVNVPSPNKAGLIA	240
Qy	241	GAIVGVLLALVLIIGLITFCQR	261

DB 241 GATIGTLALALGLIIFCCR 261

RESULT 13
US-09-997-653-505
Sequence 505, Application US/09997653
Publication No. US20030008297A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC3
CURRENT APPLICATION NUMBER: US/09/997,653

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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;

Best Local Similarity 89.3%; Pred. No. 2,36-80; Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLICVLLCGVADLTSLISITTPPEOMIEKAKETAYLPORFLGPDGSPDLIDIEWLLS 60
DB 1 MALLICVLLCGVADLTSLISITTPPEOMIEKAKETAYLPORFLGPDGSPDLIDIEWLLS 60
QY 61 PADNOKDVOYIILYSGKITYDDYQDLKGRVHFTSNLKSDDASINVTNLOLSDIGTYOC 120
DB 61 PADNOKDVOYIILYSGKITYDDYQDLKGRVHFTSNLKSDDASINVTNLOLSDIGTYOC 120
QY 121 KVKKAPGVANKKIQLTVLLKPSGTRCYVDGSEIEIGNDFKLCEPKESLPLLYEWOKLSN 180

DB 121 KVKKAPGVANKKIHLVLLVPSGARCVDGSEIEIGDFKICEPKESLPLLYEWOKLSD 180
QY 181 SQKPLTLMIAEMTSPVIVSKNASTERYSGTYSCIVKNRVSSDCLRLDVPVPSNRAGTIA 240
DB 181 SQKPLTLMIAEMTSPVIVSKNASTERYSGTYSCIVKNRVSSDCLRLDVPVPSNRAGTIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 14

US-09-993-667-505
Sequence 505, Application US/09993667
Publication No. US20030022187A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730P1C4

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: US/09/993,667

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

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PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087759

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087827

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PRIOR APPLICATION NUMBER:	60/090708
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090709
PRIOR FILING DATE:	1998-06-25

Query Match	91.1%	Score 1238;	DB 9;	Length 352;
Best Local Similarity	-89.3%;	Pred. No. 2.3e-80;		
Matches 233; Conservative	13;	Mismatches 15;	Indels 0;	Gaps 0;

QY 1 MALLTCFVLLCGVADLTRSITTPPEOMIEKAGETAYLPFCRTLPGEDEGPDIEMWLS 60
DB 1 MALLTCFVLLCGVADFPARSISITTPPEMIKAGETAYLPCKTLSPEDGPDIDIELWLS 60
QY 61 PADNOKVDQVYIIYSGDKYDDYODLKGRVHFTSNDLKSGDASINTNQLSDIGYQC 120
DB 61 PADNOKVDQVYIIYSGDKYDDYODLKGRVHFTSNDLKSGDASINTNQLSDIGYQC 120
QY 121 KVKKAPGVNKKIQLTVLLKPSGTRCYDGSSEIIGNDFKLKCEPKESGLPLYEMOKLSN 180
DB 121 KVKKAPGVNKKIHLVVLVVPKSGARCYVDGSEIIGDFKICEPKESGLPLYEMOKLSN 180
QY 181 SQKLPMTMLAEMTSPTVSVNASTSEYSGTSCYKAKRVSGDOCLLRDVPSPNAGTIA 240
DB 181 SQKLPMTMLAEMTSPTVSVNASTSEYSGTSCYKAKRVSGDOCLLRDVPSPNAGTIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 15

US-09-990-438-505
Sequence 505, Application US/09990438
Publication No. US2003002734A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1c3
CURRENT APPLICATION NUMBER: US/09/990.438
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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71	PRIOR FILING DATE: 1998-07-07

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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2,3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0

QY      1 MALLLCFVLICGVADLTRSLSTITTPBQMIKAKGETAYLPCRFITGPEODGPDLEIMLIS 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1 MALLLCFVLICGVADFPARSLSTITTPBEMI EKAKGETAYLPCRFITLSPEDGPDLEIMLIS 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      61 PADNOKVDQVILLYSGDKIYDDYODLKGRAVHTSNDLKSGDASINVTNLQSLDICTYOC 120
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DB      61 PADNOKVDQVILLYSGDKIYDDYDPDLKGRAVHTFSNDLKS GDASINVTNLQSLDICTYOC 120
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QY      121 KYKRAPGVGNKKIQTLTVLKLPSGRFCYVDGSEIENDPFLKCEPREGSLPLIYEWOKSN 180
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DB      121 KYKRAPGVANKKIHLTVLVLKPSGACVYVDGSEIEISDFKICEPKREGSLPLIYEWOKSD 180
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QY      181 SOKLPTLWLAEMTSPVISVKNASTEGSYCTVKNRNVGSDOCLRLIDVPPSNRAGTIA 240
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DB      181 SOKPETSWLAEMTSSVISVKNAASSEYSGTYSCTVKNRVGSDOCLRLINVPSPSNKAGLIA 240
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QY      241 GAVIGVLLALVILGILIFCCR 261
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DB      241 GAVIGTLLALVILGILIFCCR 261
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Search completed: July 9, 2003, 12:46:45
Job time : 26 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2003, 12:43:23 ; Search time 18 Seconds
(without alignments)
1393.949 Million cell updates/sec

Title: US-09-899-634C-2

Perfect score: 1359

Sequence: 1 MALLLCFVLLCGVADLTRSL.....AVIGVLLAVLIGLIIFCCR 261

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1270	93.5	365	2 JC7780	coxsaackie- and ade
2	196	14.4	299	2 S56749	junctional adhesio
3	159.5	11.7	4162	2 T42633	connectin/titin -
4	159	11.7	5175	2 T20992	hypothetical prote
5	159	11.7	5198	2 T43290	hemiscentin precurs
6	154	11.3	309	2 I49503	B-lymphocyte activ
7	151	11.1	7962	2 I38346	elastic titin - hu
8	144	10.6	483	2 A37821	butyrophilin - bov
9	143	10.5	483	2 T17346	hypothetical prote
10	139.5	10.3	1091	2 A58532	glial cell membran
11	136.5	10.0	518	2 JC4024	poliovirus recepto
12	136.5	10.0	3707	2 S18252	heparan sulfate pr
13	131	9.6	1323	2 PNO568	connectin 3B - chi
14	129.5	9.5	4391	2 A38096	perlecan precursor
15	128	9.4	526	2 S70887	butyrophilin precu
16	127.5	9.4	344	2 I56551	neurotrophin - rat
17	127.5	9.4	464	2 C30127	transmembrane carc
18	127.5	9.3	526	1 A32164	biliary glycoprote
19	127	9.3	509	2 JC5288	SHP substrate-1 pr
20	127	9.3	513	2 JC5289	SHP substrate-1 pr
21	127	9.3	764	2 A49448	irregular chlaem C
22	126	9.3	246	1 A32959	myelin po protein
23	124	9.1	1336	2 I60558	Fil-1 tyrosine kin
24	123.5	9.1	538	2 JC2457	vascular cell adhe
25	123.5	9.1	2222	2 T13924	sck protein - frui
26	122.5	9.0	647	2 B41288	vascular cell adhe
27	122.5	9.0	739	2 A41288	vascular cell adhe
28	122	9.0	584	2 T08678	hypothetical prote
29	121.5	8.9	738	2 A40096	platelet-endotheli

30	121	8.9	247	2 A55717	myelin/oligodendro
31	120.5	8.9	523	2 I50478	neuroilin - goldfis
32	120	8.8	811	2 A41054	fasciclin II, tran
33	120	8.8	873	2 B41054	fasciclin II pi-1i
34	119.5	8.8	392	1 RWHUPD	poliovirus recepto
35	119.5	8.8	417	1 RWHUPA	poliovirus recepto
36	119.5	8.8	1052	2 B49120	protein-tyrosine k
37	119	8.8	1896	2 T08851	Down syndrome cell
38	118.5	8.7	329	1 A48754	B7-2 antigen - hum
39	118.5	8.7	478	2 I53960	PRR2 alpha - human
40	118.5	8.7	1011	2 T13659	neuromusculin - fr
41	118	8.7	338	2 I68093	PRR2 delta - human
42	118	8.7	1033	2 S19247	cell adhesion prot
43	117.5	8.6	1176	2 JN0583	myosin-light-chain
44	116.5	8.6	333	2 A31923	amalgam protein pr
45	116.5	8.6	898	2 A40114	fasciclin II precu

ALIGNMENTS

RESULT 1

JC7780
coxsaackie- and adenovirus receptor - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #ext_change 02-Apr-2002
C/Accession: JC7780
R/Thoeien, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.
Biochem. Biophys. Res. Commun. 288, 805-808, 2001
A/Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus recept
A/Reference number: JC7780
A/Contents: Liver
A/Molecule type: mRNA
A/Residues: 1365 <THO>
A/Cross-references: GB:AY033651
C/Comment: This protein serves as the primary adenoviral attachment site on bovine cell

Query Match 93.5%; Score 1270; DB 2; Length 365;
Best Local Similarity 93.1%; Pred. No. 3e-90;
Matches 242; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY	1	MALLLCFVLLCGVADLTRSLITTPPEOMTEKAGETAYLPCRFLLGPEDGPIDEWLLS	60
DB	1	MELLRFLLCGVADTRGSLITTPPEOMTEKAGETAYLPCRFLLGPEDGPIDEWLLS	60
QY	61	PADNQRVDYIIYSGDKYDDYDYLKGRVHFTSNDLKSASINVTNLQSLDIGTYQC	120
DB	61	PADNQRVDYIIYSGDKYDDYDYLKGRVHFTSNDLKSASINVTNLQSLDIGTYQC	120
QY	121	KVKKAGVGNKKIQLTVLKPSTRCYVDSSEISGNDPFLKCPKRGSLPLVEMOKLSN	180
DB	121	KVKKAGVGNKKIQLTVLKPSTRCYVDSSEISGNDPFLKCPKRGSLPLVEMOKLSN	180
QY	181	SGKLPTLMLAEMTSPVIVSNASTESGYSCVTKRVGSDQCLRLDVVPSPNRACTIA	240
DB	181	SGKLPTSLPEMSPVIVSNASTESGYSCVTKRVGSDQCLRLDVVPSPNRACTIA	240
QY	241	GAVIGVLLAVLIGLIIFCCR	260
DB	241	GAVIGVLLAVLIGLIIFCCR	260

RESULT 2
S56749
junctional adhesion molecule precursor - human
N/Alternate names: Fli platelet antigen; platelet adhesion molecule PAM-1; platelet Fli
C/Species: Homo sapiens (man)
C/Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #ext_change 01-Feb-2002
C/Accession: A59406; S56749
R/Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.;
J. Immunol. 163, 553-557, 1999
A/Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribut

R,Vogel, B.E.; Hedgecock, E.M.
 Submitted to the EMBL Data Library, June 1998
 A:Description: Hemiscentin is required for hemidesmosome mediated cell adhesion and germ-
 A:Reference number: 222396
 A:Accession: T43290
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-5198 <VOG>
 A:Cross-references: EMBL:AF074901; PIDN:AA26792.1
 R:Stalson, J.
 Submitted to the EMBL Data Library, December 1994
 A:Reference number: Z1935
 A:Accession: T20993
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5198 <WIL>
 A:Cross-references: EMBL:Z47066; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F1569.4b
 A:Experimental source: clone F15G9
 R:Kerhaw, J.
 Submitted to the EMBL Data Library, December 1994
 A:Reference number: Z19929
 A:Accession: T24734
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5198 <W12>
 A:Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F1569.4b
 A:Experimental source: clone T09B9
 C:Genetics:
 A:Gene: him-4; F15G9.4b
 A:Map position: X
 A:Intons: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
 ; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
 1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/
 Query Match 11.7%; Score 159; DB 2; Length 5198;
 Best Local Similarity 25.4%; Pred. No. 0.0022;
 Matches 68; Conservative 32; Mismatches 92; Indels 76; Gaps 12;
 QY 12 GVADLFRSLSTITPEQMI-----KAKGETAVLPCEFTGPEDEGDLDEMLSPADNQ 65
 DB 3845 GVALELVLDVFPFPPVSVSNDPINALGETITLFCASGNPVPQ-----LKW----- 3892
 QY 66 KVDQVILVSGDKIYD---YYODLKGRVHTSNDLKSQDASINVTNLQSLDITGYCKV 122
 DB 3893 -----AKGSLIFPSPDGRARISLKG-----ARLDIPHLKKTVDGDTYCCQ 3932
 QY 123 KKAPEGNNKKIQLTLVLLKPGCTRCYVDGSEIGNDFLKCPEKPGSLPLLYEMQKLSNQ 182
 DB 3933 LNAAGTSEASVSVDVLPPEINRDGIDMSPL-----PAQOSLTL-----QCLAQCK 3979
 QY 183 KLPTL-WLAEMT-----SPVTSVKNASTREVSCTYKNNVSGSDQCLRL 227
 DB 3980 PVIQMRKTLNGTALTHTSTPGITVASDSTFIQINNVSLSKGVYTCIAENVAGSDNLMYVY 4039
 QY 228 DVV--PPSNRAGT---IAG--AVIGVL 248
 DB 4040 DVQAPVINSNGTKQVIEGLAVIECLV 4067
 RESULT 6
 I49503
 B-Lymphocyte activation antigen 7 precursor - mouse
 N:Alternate names: MB7-2
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
 C:Accession: I49503; S17291; I49521
 R:Selvakumar, A.; White, P.C.; Dupont, B.
 Immunogenetics 38, 292-295, 1993
 A:Title: Genomic organization of the murine B-Lymphocyte activation antigen B7.
 A:Reference number: I49503; MUID:9330789; PMID:766531
 A:Accession: I49503
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-309 <RES>
 A:Cross-references: GB:L12589; NID:g293299; PIDN:AAA7240.1; PID:g293301
 R:Freeman, G.J.; Gray, G.S.; Gimm, C.D.; Lombard, D.B.; Zhou, L.J.; White, M.; Fingero
 J. Exp. Med. 174, 625-631, 1991
 A:Title: Structure, expression, and T cell costimulatory activity of the murine homolo
 A:Reference number: S17291; MUID:91341422; PMID:1714935
 A:Accession: S17291
 A:Molecule type: mRNA
 A:Residues: 1-274; R', 279-309 <PRE>
 A:Cross-references: EMBL:X60958; NID:g50111; PIDN:CAA43291.1; PID:g50112
 R:Inoue, M.; Linley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Ueda, T.
 Biochem. Biophys. Res. Commun. 200, 443-449, 1994
 A:Title: Identification of an alternatively spliced form of the murine homologue of B7.
 A:Reference number: I49521; MUID:94220123; PMID:7513163
 A:Accession: I49521
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-143; 238-274; R', 279-309 <RE2>
 A:Cross-references: GB:D16220; NID:g505118; PIDN:BA03748.1; PID:g994769
 C:Genetics:
 A:Gene: B7
 A:Intons: 37/1; 143/1; 237/1; 275/1
 C:Superfamily: B-Lymphocyte restricted antigen B7
 C:Keywords: alternative splicing
 Query Match 11.3%; Score 154; DB 2; Length 309;
 Best Local Similarity 22.9%; Pred. No. 0.00017;
 Matches 65; Conservative 55; Mismatches 108; Indels 56; Gaps 13;
 QY 3 LLLFVLLCGVADLFRSLSTITPEQMIERAKGETAVLPCEFTGPEDEGDLDEMLSPA 62
 DB 21 LILLFVLLRLSGVSSDV-----DEQLSKSVKDKVLLPCRYNSPHDESDRIYV----- 70
 QY 63 DNGKVDQVIL-LYSGD-KIYDDYODLKGRVHTSNDLKSQDASINVTNLQSLDITGYCC 120
 DB 71 --QKHQVAVLSVAGLKWPEY---KRRITLYDNTY---SLIILGLVSDRGTYSC 119
 QY 121 KYKAPGVGNKKIQLTLVLLKPS-----GTRCYVDGSEIGNDFLKCPEKPGSLPLLYEM 175
 DB 120 VVQKER-GTYEVKHALVLRSLKADFTSPNITESGNPDAFTKRTICFASGEPKRFWS 178
 QY 176 QKLSNQKLPTLWLAEMTSPVTSVKNAST-EYSGTCTYKNNVSGSDQCLRL----- 227
 DB 179 --LENGRELPGINTTISQPESELTYTSSQLDENTRNTIK-----CLIKYGAHVS 229
 QY 228 -----DVPPSNRAGTIAVIGVLLAVLIGLIFC-CR 261
 DB 230 EDFTEKPEPDPDSKNTLVLFAGFGAVITVIVIIKCFCK 273
 RESULT 7
 I38346
 elastic titin - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
 C:Accession: I38346
 R:Labat, S.; Kolmerer, B.
 Science 270, 293-296, 1995
 A:Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
 A:Reference number: A57430; MUID:96026330; PMID:7569978
 A:Accession: I38346
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-7962 <RES>
 A:Cross-references: EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017427
 A:Gene: GDB:TTN
 A:Cross-references: GDB:127867; OMIM:188840
 A:Map position: 2q31-2q31
 Query Match 11.1%; Score 151; DB 2; Length 7962;
 Best Local Similarity 23.9%; Pred. No. 0.015;
 Matches 61; Conservative 31; Mismatches 77; Indels 86; Gaps 12;

Qy	12	GVADLTRSLSTTP-----BQMEKAGETAUVECRTLGPEODG---PLDIEMTLSPAD	63
Db	4050	GSASSSTSLKKEPPIFFKKPHPIETTLKGADVHLEC-----ELQGTPEPHVSN-----	4097
Qy	64	NQKVDVUUIIYSGDKIYDDYQDLKGRVHTSNLKSGD-----ASINVTNQLS	113
Db	4098	-----YKD-----KRELRSGKKYKIMSENFLTIIHILNVDA	4129
Qy	114	DIGTYOCKVKKAPGVGNKKIQLTVLTK--PQSTRVYVGSGEIGNDFLTKKEPREGSLPL	171
Db	4130	DIGETÖCKATN--DVGSDTCVGSIALKPAPRFVKLDSISTYVGKEVQLÖ--TTLEGAPFI	4186
Qy	172	LYEMOK-----LNSOQLPTLMLAEMTSPVIVSNASTEXSGTYSCTVKNRV	218
Db	4187	SVWFVKDKGEIVRESDNIMWISYSENIATLQFSR-----VEPANA-----GKVTQCKRDA	4236
Qy	219	GSDQCLRLDLYVPPS	233
Db	4237	GMÖCEFATLSVLEPA	4251

RESULT 8
A37821
butyrophilin - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 05-Nov-1999
C:Accession: A37821
R:Jack, L.J.W.; Mather, I.H.
J Biol. Chem. 265, 14481-14486, 1990
A:Title: Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycoprotein
A:Reference number: A37821; MUID:90354441; PMID:2387867
A:Accession: A37821
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-526 <JAC>
A:Cross-References: GB:M5551; NID:g1763685; PIDN:AAB39766.1; PID:g162773
C:Keywords: transmembrane protein

Query Match	10.6%	Score 144	DB 2	Length 526
Best Local Similarity	23.4%	Pred. No. 0.0019		
Matches	67	Conservative	50	Mismatches 113, Indels 56, Gaps 13,
QY	4	LLCFLVLLCGVADLTNLSITTPQOMIEKAKGETAYLPCRFTLGPDGGLDIEML--LS	60	
DB	13	LLIIFLITDLPKLDASAPFDVIGPQEBITLAVVGGEDALPCRLSNNVASAK-MELRMWRERKVS	71	
QY	61	PADNOKVDQVILLYSGDKLYDDYODLGRVHFTFNDLKSQASINVTNLQISDITGYOC	120	
DB	72	PA-----VFVSRGQGEQGEEMAEYGRVSLVSDHIAEGSVANRIQEVASDDGEVRC	124	
QY	121	KVKKAPGVGNKKIQTLTLIKPSGTRCYVDGSEIENDFLKC-----EPK-----EG	167	
DB	125	FFRQDENYEALIVHLKV--AALGSPHISMKVQSGEIQLEBTSVGWYPERDQWRTHRG	182	
QY	168	SLPLLEWQKLSNQSKLPTLWLAEMTSPV-----SVKASTEYSGVCTVKN-RVGSQD	222	
DB	183	E-----EFPMSSESNPDBEGFLTYRASVILRDSMKRV-----SCCIRNLLLGQEK	229	
QY	223	CLLRIDV---VP-----PSNRAGTINGANIYGVLLALVLGLITFCRC	261	
DB	230	-----DVEVSIIPASEFPRLTPMWWAAVAILVVLGLITGSGIFFTFR	270	

RESULT 9
T17346
hypothetical protein DKFZ58601624.1 - human (Fragment)
CtSpecies: Homo sapiens (man)
CtDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 15-Oct-1999
CtAccession: T17346
R.Duisterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999

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A:Reference number: Z18727
A:Accession: T17346
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-483 <DUE>
A:Cross-references: EMBL:AL117666
A:Experimental source: adult uterus; clone DKFZ58601624
C:Genetics:
A>Note: DKFZ58601624.1

Query Match      10.5%; Score 143; DB 2; Length 483;
Best Local Similarity 26.3%; Pred. NO. 0.0021;
Matches 41; Conservative 31; Mismatches 80; Indels 4; Gaps 3

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Oy      10  VTNLQSDJDTGVOCKVKKAPGVGNKKIQLTVLTKSGTRCYVDSGEELGDNFKLCEPKK 166
      11  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      49  ITDKIKDDGCVISCTAQNQSAGISANATTVLETPSLVPELDRVSVGEIVALQCK-AT 107
Oy      167 GSPLLYEWOKLSNSQKLEPTLWLAEMTSPVISVKNASTREVSAGTSCYVKNRQVSDOCLIR 226
Db      108 GNPPEPRITWFKGDRPISLTERHHLLTPDQDLVQNVAVEDGRTCEMSNTLGERASHQ 167
Oy      227 LDVPPS--NRAGTIGA-VIGVLLVALIGLIIFC 259
Db      168 LSVLPAAQCKQDTYIGITIVAVSVIUTSLVWC 203

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RESULT 10
A58532
Glial cell membrane glycoprotein LIG-1 precursor - mouse
CISpecies: Mus musculus (house mouse)
CDate: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 05-Nov-1999
CAccession: A58532
R:Suzuki, Y.; Sato, N.; Tohyama, M.; Wanaka, A.; Takagi, T.
J. Biol. Chem. 271, 22522-22527, 1996
A>Title: cDNA cloning of a novel membrane glycoprotein that is expressed specifically in
AReference number: A58532, MUID:96394313, PMID:8798419
AAccession: A58532
AStatus: preliminary; translated from GB/EMBL/DBD

A:Residues: 1:1091 <SUZ>
A:Cross-references: GB:D8572; NID:g1545806; PIN:BA11416.1; PID:g1545807
C:Subfamily: leucine-rich alpha-2-glycoprotein repeat homology: proteoglycan amino-te
F:35-61/Domain: leucine-rich alpha-2-glycoprotein repeat homology <RAH>
F:71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F:75-117/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:118-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:142-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F:166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F:191-213/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F:214-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F:238-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F:262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F:286-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F:310-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F:334-357/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F:358-381/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F:382-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F:409-433/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F:440-485/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match	10.3%	Score 139.5;	DB 2;	Length 1091;
Best Local Similarity	22.0%;	Pred. No. 0.01;		
Matches 55; Conservative	37;	Mismatches 106;		Indels 31;
				Gaps 9

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QY      34  GEAIVLPCRRITLAPPEQGLDIEMLSPADNKKVQVILVSGMDIVDYDQADKGRVNF  93
Db      615  GTTARLECAATGHPNQ-----IAM-----QK-----DGG--TDFAARERMHV  655
QY      94  TSNDSKSGDASIVNTNLQSDIGTQYCKKKAPGVGNKKIQLTVLAKRSGRCRVYDQSEE  155
Db      653  MPDQ---DVFF-IITVKKIDMGVYSCTAQNNSAGSVANATLTVLETSTSLAVPLEDRVVT  707

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QY 154 IGDPLKKEPKKSGSLPLYEWOKLSQQLPTLWLAEMTSPIVSKASTEYSGTSC 213
 Db 708 VGETVAFQCKATGSPPTPRI-TWLKGRPLSLTERHFTPNQNLVQNVIMIDAGRYTCE 766
 QY 214 VKRNVSDQCLRLDVVP--SNRAGTIAGA-VIGVLLAVLGLIIFC 259
 Db 767 MSNPLGTERAHQSILPTPGCKRKGDTTGVIGFTIIVACISVLISLWVC 815

RESULT 11

JC4024
 poliovirus receptor-related protein precursor - human

C/Species: Homo sapiens (man)

C/Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999

C/Accession: JC4024

R/Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubd

Gene 155, 261-265, 1995

A/Title: Complementary DNA characterization and chromosomal localization of a human gene

A/Reference number: JC4024; MUID:95237621; PMID:7721102

A/Accession: JC4024

A/Molecule type: mRNA

A/Residues: 1-518 <LOP>

A/Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796

C/Genetics:

A/Gene: GDB:PVRR1

A/Cross-references: GDB:583951

A/Map position: 11q23-11q24

C/Superfamily: poliovirus receptor; immunoglobulin homology

C/Keywords: glycoprotein; transmembrane protein

F/1-30/Domain: signal sequence #status predicted <SIG>

F/31-518/Product: poliovirus receptor-related protein #status predicted <MAT>

F/356-379/Domain: transmembrane #status predicted <TM>

F/36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.0%; Score 136.5; DB 2; Length 518;

Best Local Similarity 18.5%; Pred. No. 0.0072;

Matches 67; Conservative 50; Mismatches 86; Indels 159; Gaps 17;

QY 34 GETAVLPICRFTLPEDQGLDIEWLSPADNOKVDV-----ILYS--GDK 78

Db 44 GTDVLHCSFA-----NPLPSVKITQVTMOKSTNGKONVAITNPSMGVS 88

QY 79 IYDDYQDLKGRVHTSNLKSGDASINVTNQLSDIGTYQCKVKAPGVGNKKIQ--LT 136

Db 89 VLAPY-----REVFELRPST--DGTIRLSLELEDGVIYCEPATRP--TGNRESQNL 141

QY 137 VLKPSGSTRGVNDSSEI-----GNPKL--KCEPKESGLPLYEWQ-KLSNSQKLP-- 185

Db 142 VMKPTN--WIEGTAQLRAKKGQDDKLVATCTSANGRPVSVMETRLKGEARVPGD 198

QY 186 -----TWLAEMTSPIVSKN----- 201

Db 199 SGTPMAVTVISRYRLVPSREAHQSLACIVNTHMDFKESLTINVQYEPVETIEGDGN 258

QY 202 -----ASTEY-----SGTYSCT 213

Db 259 WYLQRMVDVLTCKADANPATEYHMTLNSLPKGEAQNRTLEFKSPIYSLAGTYICE 318

QY 214 VKRNVSDQCLRLDVVP-----PPSN--RAGTIAGAVIG-----VLALVLLGLIIFC 259

Db 319 ATNPITGRSGVEVNITEPPTSPPEHGRAGVPFAIIGVAGSILVLIIVGVGIVVA 378

QY 260 CR 261

Db 379 LR 380

RESULT 12

S18252
 heparan sulfate proteoglycan - mouse

N/Alternate names: perlecan

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C/Accession: S18252; A31917; B31917; S66460
 R/Noonan, D.M.; Fullie, A.; Valente, P.; Cal, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; H
 J. Biol. Chem. 266, 22939-22947, 1991

A/Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteog
 adhesion molecule.

A/Reference number: S18252; MUID:92078153; PMID:1744087

A/Accession: S18252

A/Molecule type: mRNA

A/Residues: 1-3707 <NOO>

A/Cross-references: EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g200296

R/Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogel, G.; Sasaki, M.; Yamada, Y.; Has

J. Biol. Chem. 263, 16379-16387, 1988

A/Title: Identification of cDNA clones encoding different domains of the basement membr-

A/Reference number: A92680; MUID:89034110; PMID:2972708

A/Accession: A31917

A/Molecule type: mRNA

A/Residues: 940-1601 <NO2>

A/Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253

A/Accession: B31917

A/Molecule type: mRNA

A/Residues: 1870-2600 <NO3>

A/Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301

R/Schulze, B.; Mann, K.; Batschutt, R.; Wiedemann, H.; Timpl, R.

Eur. J. Biochem. 231, 551-556, 1995

A/Title: Structural properties of recombinant domain III-3 of perlecan containing a gloi

A/Reference number: S66460; MUID:95377282; PMID:7649154

A/Accession: S66460

A/Molecule type: protein

A/Residues: 1272-1274, 'X', 1276, 'X', 1278-1279 <SCH>

C/Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G rep-

C/Keywords: glycoprotein

F/199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F/285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F/325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F/368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F/764-811/Domain: laminin-type EGF-like homology <LEG3>

F/1559-1206/Domain: laminin-type EGF-like homology <LEG7>

F/1563-1610/Domain: laminin-type EGF-like homology <EG7>

F/1613-1668/Domain: laminin-type EGF-like homology <EG8>

F/3163-3198/Domain: EGF homology <EGF>

F/3270-3423/Domain: laminin G repeat homology <LG>

F/3464-3482/Domain: EGF homology <EGF7>

F/1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicte

Query Match 10.0%; Score 136.5; DB 2; Length 3707;

Best Local Similarity 21.3%; Pred. No. 0.079;

Matches 61; Conservative 38; Mismatches 102; Indels 85; Gaps 12;

QY 20 LSTTPQWIEKAGETAVLPICRFTLPEDQGLDIEWLSPADNOKVDVITLYSGDKI 79

Db 2346 ISIEPPSSIVQ--QGDDAFKC--LIHGGAMPKIVEMKI--RDQLEENVHISPPGSI 2398

QY 80 -----YDDY--QDL-----KGRVH-----FTSNDLK 99

Db 2399 TIVAPGATMEPTACVANSVYGAQGVNLSVHGPTVSVLDEGPVHVMKGDITTECIS 2458

QY 100 SGD-----ASINVTNQLSDIGTYQCKVKAPGVGNK 132

Db 2459 SCEPRSSPMTWLIGIVKLEPRMFGIMNSHAMIKLASVPSDGIYVCAQONLGAQKQ 2518

QY 133 IQLTV--LLKPSGTRCYVDGSE--EIGNDFLKCEPKESGLPLYEWOKLSNSQKLP 186

Db 2519 VELIVDTGVAPQETPVQVBEBSLTLIEAGHTATLHKS-ATGNPPTIHHSKL----RAPL 2573

QY 187 LWLAEMTSPIVSKASTEYSGTYSCTVKNRVGSDQCLRLDVVP 232

Db 2574 PMQHRIGENTLIVIPRAVQODSGOYICNATNSAGHTEATVVLHVESP 2619

RESULT 13

PN0568
 connectin 3B - chicken (fragment)

N/Alternate names: Cn3b protein

A:Accession: A41059
A:Molecule type: mRNA
A:Residues: 'RT',892-908,'R',910-1101,'L',1103-1132,'L',1134-1221,'L',1223-1397 <KA2>
A:Cross-references: GB:Sf6436; NID:g9243370; FIDN:AAE1121.1; PID:g243371
R:Dodghe, G.R.; Kovalevsky, I.; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Iozzo, R.
Genomics 10, 673-680, 1991
A:Title: Heparan sulfate proteoglycan of human colon: partial molecular cloning, cellular
A:Reference number: A40306; MUID:91365376; PMID:1679749
A:Accession: A40306
A:Molecule type: mRNA
A:Residues: 1018-1405,'G',1407-1409,'G',1411-1465 <DOD>
A:Cross-references: GB:M64283; NID:g184424; PIDN:AA52699.1; PID:g184425
R:Heremans, A.; van der Schueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van der
J. Cell Biol. 109, 3199-3211, 1989
A:Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclonal
antibodies.
A:Reference number: A33625; MUID:90078352; PMID:2687294
A:Accession: B33625
A:Molecule type: protein
A:Residues: 1379-1384,'X',1386-1388,'X',1390-1398 <HE2>
A:Accession: A33625
A:Molecule type: protein
A:Residues: 2166-2171,'X',2173-2175,'X',2177-2185 <HE3>
A>Note: peptide potentially matches four different regions of sequence shown
C:Genetics:
A:Gene: GDB:HSRPG2
A:Cross-references: GDB:126372; OMIM:142461
A:Map position: 1p36.1-1p36.1
C:Keywords: chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmembrane
F:1.21/Domain: signal sequence #status predicted <SIG>
F:22-4391/Product: perlecan #status predicted <MAT>
F:122-139/Domain: I <DOM1>
F:194-530/Domain: II <DOM2>
F:199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:531-1676/Domain: III <DOM3>
F:1159-1206/Domain: laminin-type EGF-like homology <LEG>
F:1663-1610/Domain: laminin-type EGF-like homology <EG7>
F:1613-1666/Domain: laminin-type EGF-like homology <LEG8>
F:1677-3686/Domain: IV <DOM4>
F:2007-2034/Domain: transmembrane #status predicted <TRM>
F:3687-4391/Domain: V <DOM5>
F:3845-3880/Domain: EGF homology <EGF1>
F:3888-3921/Domain: EGF homology <EGF>
F:3853-4106/Domain: laminin G repeat homology <LG2>
F:4147-4175/Domain: EGF homology <EGF2>
F:4149-4151/Region: motor neuron attachment (L-R-E) motif
F:4159-4301/Region: motor neuron attachment (L-R-E) motif
F:4593-4610/Region: motor neuron attachment (L-R-E) motif
F:65,71,76/Binding site: heparan sulfate (Ser) (covalent) #status predicted
F:89,554,1055,2121,3105,3279,3780,3836,4068/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:2295,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 12:42:08 ; Search time 10 Seconds
(without alignments)
1082.532 Million cell updates/sec

Title: US-09-899-634C-2

Perfect score: 1359

Sequence: 1 MALLCFVLLCGVADLTRSL.....AVIGVLLVLIIGLIIFCCR 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	91.1	365	1	CXAR_HUMAN
2	1216	89.5	365	1	CXAR_MOUSE
3	351.5	25.9	319	1	A33_HUMAN
4	196	14.4	299	1	JAMI_HUMAN
5	181.5	13.4	298	1	JAMI_HUMAN
6	171	12.6	298	1	JAMI_BOVIN
7	161.5	11.9	300	1	JAMI_MOUSE
8	154	11.3	306	1	CD80_MOUSE
9	144	10.6	526	1	BUTY_BOVIN
10	136.5	10.0	740	1	PECI_PIG
11	136.5	10.0	3707	1	PGBM_MOUSE
12	132	9.7	517	1	PVRI_HUMAN
13	131.5	9.7	348	1	KILO_RAT
14	129.5	9.5	515	1	PVRI_PIG
15	128.5	9.5	4393	1	PGBM_HUMAN
16	128	9.4	526	1	BUTY_HUMAN
17	127.5	9.4	344	1	NTRI_RAT
18	127.5	9.4	526	1	CEAL_HUMAN
19	127	9.3	764	1	ICCR_DROME
20	126	9.3	246	1	MYPO_HETFR
21	125.5	9.2	727	1	PECI_MOUSE
22	124	9.1	1336	1	VCAI_RAT
23	122.5	9.0	739	1	VCAI_HUMAN
24	121.5	8.9	738	1	PECI_HUMAN
25	120.5	8.9	515	1	PVRI_MOUSE
26	120.5	8.9	555	1	C166_CARAU
27	120	8.8	246	1	MOG_MOUSE
28	120	8.8	837	1	NCM2_HUMAN
29	120	8.8	873	1	FAS2_DROME
30	119.5	8.8	245	1	MOG_RAT
31	119.5	8.8	417	1	PVR_HUMAN
32	119.5	8.8	1052	1	FGR2_DROME
33	119	8.8	2012	1	DSCA_HUMAN

RESULT 1

ID	CXAR_HUMAN	STANDARD;	PRT;	365 AA.
AC	P78310; C00694;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Coxsackievirus and adenovirus receptor precursor (Coxsackievirus B-adenovirus receptor) (hCAR) (CVB3 binding protein).			
GN	CXADR OR CAR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97190109; PubMed=9036860;			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,			
RA	Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;			
RT	"Isolation of a common receptor for Coxsackie B viruses and			
RT	adenoviruses 2 and 5."			
RL	Science 275:1320-1323(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97250541; PubMed=9096397;			
RA	Tomko R.P., Xu R., Philipson L.;			
RT	"HCAR and MCAR: the human and mouse cellular receptors for subgroup C			
RT	adenoviruses and group B coxsackieviruses."			
Proc.	Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20008750; PubMed=10543405;			
RA	Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,			
RA	Bowles N.E.;			
RT	"Genomic organization and chromosomal localization of the human			
RT	Coxsackievirus B-adenovirus receptor gene."			
Hum. Genet.	105:354-359(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;			
RT	"Sequence and expression of CXADR, the human gene for the			
RT	coxsackievirus and adenovirus receptor."			
Submitted	(Oct-1999) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND			
CC	SUBGROUP C ADENOVIRUSES (AD2 AND AD5).			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.			
CC	-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.			
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ALIGNMENTS

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CC -----
DR EMBL; Y07593; CAA68868.1; -.
DR EMBL; U90716; AAC51234.1; -.
DR EMBL; AF169366; AAF05908.1; -.
DR EMBL; AF169360; AAF05908.1; JOINED.
DR EMBL; AF169361; AAF05908.1; JOINED.
DR EMBL; AF169362; AAF05908.1; JOINED.
DR EMBL; AF169363; AAF05908.1; JOINED.
DR EMBL; AF169364; AAF05908.1; JOINED.
DR EMBL; AF169365; AAF05908.1; JOINED.
DR EMBL; AF200465; AAF24344.1; -.
DR EMBL; HGNC:2559; CXADR.
DR MIM; 602621; -.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003598; Iq_c2.
DR InterPro; IPR003600; Iq_like.
DR Pfam; PF00047; Iq; 2.
DR SMART; SM00410; Iq_Like; 1.
DR SMART; SM00408; IGG2; 1.
DR Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 365 COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.
FT DOMAIN 20 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 258 POTENTIAL.
FT DOMAIN 259 365 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 34 127 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 155 219 IG-LIKE C2-TYPE DOMAIN 2.
FT DISULFID 41 120 BY SIMILARITY.
FT DISULFID 162 212 BY SIMILARITY.
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 365 AA; 40029 MW; AB01C6346CB7FE64 CRC64;

Query Match 91.1%; Score 1238; DB 1; Length 365;
Best Local Similarity 89.3%; Pred. No. 5.7e-96;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCFVLGCGVADLTRSLITTPQEMIEKAGETAYLPCRFTLGPEDQGLDIEWLLS 60
DB 1 MALLLCFVLGCGVDFARSLSITTPQEMIEKAGETAYLPCRFTLGPEDQGLDIEWLLS 60
QY 61 PADNQNQVDQVILLYSGDKIYDDYQDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQC 120
DB 61 PADNQNQVDQVILLYSGDKIYDDYQDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQC 120
QY 121 KVKAPGVGNKIQLTVLLKPSGTRCYVDGSEIEGNDPFLKCRPKGSLPLLYEWQKLSN 180
DB 121 KVKAPGVGNKIHVLVLPSPGARCVDGSEIEGSDFKIKCEPKGSLPLQYEWQKLSN 180
QY 181 SOKLPTLWLAEMTSPLVSVKNASTEYSGTYSCTVKNRVGSDQCLLRDLVVPPSNRAGTIA 240
DB 181 SQKMTPLWLAEMTSPLVSVKNASTEYSGTYSCTVKNRVGSDQCLLRDLVVPPSNRAGTIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 2
CXAR MOUSE STANDARD; PRT; 365 AA.
AC P97752; O09052;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coxsackievirus and adenovirus receptor homolog precursor (mCAR).
GN CXADR OR CAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
AN [1]
```

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RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Liver;
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Coxsackie B viruses and
RT adenoviruses 2 and 5."
RL Science 275:1320-1323(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/MAI;
RC MEDLINE=97190109; PubMed=9036860;
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Coxsackie B viruses and
RT adenoviruses 2 and 5."
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA Bergelson J.M., Krithivas A., Crowell T.L., Finberg R.W.;
RT "The murine CAR homologue (mCAR) is a receptor for coxsackie B
RT viruses and adenoviruses."
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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CC -----
DR EMBL; Y10320; CAA71368.1; -.
DR EMBL; U90715; AAC53148.1; -.
DR EMBL; Y11929; CAA72679.1; -.
DR MGD; MGI:1201679; Cxadr.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003598; Iq_c2.
DR InterPro; IPR003600; Iq_Like.
DR Pfam; PF00047; Iq; 2.
DR SMART; SM00410; Iq_Like; 1.
DR SMART; SM00408; IGG2; 1.
DR Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 365 COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.
FT DOMAIN 20 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 258 POTENTIAL.
FT DOMAIN 259 365 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 34 127 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 155 219 IG-LIKE C2-TYPE DOMAIN 2.
FT DISULFID 41 120 BY SIMILARITY.
FT DISULFID 162 212 BY SIMILARITY.
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 340 365 VV (IN REF. 2 AND 3).
SQ SEQUENCE 365 AA; 39947 MW; 5445B4B52A34B2A2 CRC64;

Query Match 89.5%; Score 1216; DB 1; Length 365;
Best Local Similarity 88.1%; Pred. No. 3.9e-94;
Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MALLLCFVLGCGVADLTRSLITTPQEMIEKAGETAYLPCRFTLGPEDQGLDIEWLLS 60
DB 1 MALLLCFVLGCGIADFTSGLSITTPQREKAGETAYLPCRFTLGPEDQGLDIEWLLS 60
QY 61 PADNQNQVDQVILLYSGDKIYDDYQDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQC 120
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Db 61 PSDNQIVQVILYSGDKIYDNYPPDLKGRVHTSNDVKSGDASINVTNLQSLDIGTYQC 120
Qy 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFKLCBPKESLPLLYEWOKLSN 180
Db 121 KVKKAPGVANKKELLTVLVKPSGTRCFVDSGEIIGNDFKLCBPKESLPLQFEWOKLSD 180
Qy 181 SOKLPTLWLAEMTSPVISVKNASTEYSGTCTVKNRVGSDQCLLRDLVVPSPNRAAGTIA 240
Db 181 SOTMPTPLWLAEMTSPVISVKNASSEYSGTCTVQNRVGSQDQMLRLDVVPSPNRAAGTIA 240
Qy 241 GAVIGVLLALVLIIGLIIFCC 260
Db 241 GAVIGTLLALVLIIGLIIFCC 260

RESULT 3
A33_HUMAN
ID A33_HUMAN STANDARD; PRT; 319 AA.
AC Q99795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cell surface A33 antigen precursor (Glycoprotein A33).
GN GPA33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Colon carcinoma;
RX MEDLINE=97165045; PubMed=9012807;
RA Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
RA Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
RA Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
RA Burgess A.W.;
RT "The human A33 antigen is a transmembrane glycoprotein and a novel
RT member of the immunoglobulin superfamily.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:469-474 (1997).
RN [2]
RP POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=9736159; PubMed=9245713;
RA Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
RA Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
RA Simpson R.J.;
RT "Characterization of posttranslational modifications of human A33
RT antigen, a novel palmitoylated surface glycoprotein of human
RT gastrointestinal epithelium.";
RL Biochem. Biophys. Res. Commun. 236:682-686 (1997).
CC -1- FUNCTION: MAY PLAY A ROLE IN CELL-CELL RECOGNITION AND SIGNALING.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN NORMAL GASTROINTESTINAL
CC EPITHELIUM AND IN 95% OF COLON CANCERS.
CC -1- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 K OF N-LINKED
CC CARBOHYDRATE.
CC -1- PTM: PALMITOYLATED.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
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CC -----
CC EMBL; U79725; AAC50957.1; --
CC GenBank; HGNC:4445; GPA33.
CC MIM; 602171; --
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003600; Ig_like.

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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00410; IG like; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
KW Transmembrane; Signal; Antigen.
FT SIGNAL 1..21
FT CHAIN 22..319 CELL SURFACE A33 ANTIGEN.
FT DOMAIN 22..235 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 236..256 POTENTIAL.
FT DOMAIN 257..319 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 36..124 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 139..229 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 258..261 POLY-CYS.
FT DISULFID 43..117 POTENTIAL.
FT DISULFID 146..222 POTENTIAL.
FT DISULFID 162..211 POTENTIAL.
FT CARBOHYD 112..112 N-LINKED (GLCNAC. . .).
FT CARBOHYD 200..200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223..223 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AAF45C2408E CRC64;

Query Match 25.9%; Score 351.5; DB 1; Length 319;
Best Local Similarity 34.1%; Pred. No. 3.9e-22;
Matches 89; Conservative 53; Mismatches 96; Indels 23; Gaps 11;

Qy 10 LCGVADLTRSLSTTPEQMIKAKGETAYLPCRFTLGPEDQGPLDIEM---LLSPADNOK 66
Db 12 LCAVRVTVDIAISVETPDQVLRASQKSVTLPTCTYHTSTSSRECL-IQWKLILT-----H 65
Qy 67 VQVILYSGDK--YDDYYQDLKGRVHTSNDLKSQDASINVTNLQSLDIGTYQCKVK 124
Db 66 TERVVIWPFPSKNYIHGELY---KNRVSI-SNNAEQSDASITIDQLTMADNGTYECSVL 121
Qy 125 APGV-GNKK--IQLTVLLKPSGTRCYVDGSEIIGNDFKLCBPKESLPLLYEWOKLS-N 180
Db 122 MSDLEGNTKSRVLLVLPVPSKPECGIETIGTIGNNIQLTCSKESGPTTPQYSWKRYNIL 181
Qy 181 SOKLPTLWLAEMTS-PVISVKNASTEYSGTCTVKNRVGSDQCLLRDLVVPSPNRAAGTI 239
Db 182 NQEQP---LAQPASGQPVSLKNISTDTSGYICTSSNEEGTQFCNITVAVRSPSMVALY 238
Qy 240 AGAVIGVLLALVLIIGLIIFCC 260
Db 239 VGIVAGVVAALIIGIIGIYCC 259

RESULT 4
JAM1_HUMAN
ID JAM1_HUMAN STANDARD; PRT; 299 AA.
AC Q9Y624;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Junctional adhesion molecule 1 precursor (JAM) (Platelet adhesion
DE molecule 1) (PAM-1) (Platelet F11 receptor).
GN JAM1 OR JCAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99323940; PubMed=10395639;
RA Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA Iwamatsu A., Kita T.;
RT "Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes
RT redistribution of junctional adhesion molecule in human endothelial
RT cells.";
RL J. Immunol. 163:553-557 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss C.,

```


DE Junctional adhesion molecule 1 precursor (JAM).
GN JAM1 OR JCAM1 OR JCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98327120; PubMed=9660867;
RA Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
RA Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
RA Simmons D., Dejana E.;
RT "Junctional adhesion molecule, a novel member of the immunoglobulin
RT superfamily that distributes at intercellular junctions and modulates
RT monocyte transmigration.";
RL J. Cell Biol. 142:117-127(1998).
CC -!- FUNCTION: PLAYS A ROLE IN REGULATING MONOCYTE TRANSMIGRATION
CC -!- INVOLVED IN INTEGRITY OF EPITHELIAL BARRIER. INVOLVED IN PLATELET
CC ACTIVATION.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: LOCALIZED AT TIGHT JUNCTIONS OF BOTH
CC EPITHELIAL AND ENDOTHELIAL CELLS.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U89915; AAC32982.1; --
CC MGD; MGI:1321398; Jcam1.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003600; Ig_Like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00410; Ig_Like; 1.
CC SMART; SM00406; IG; 1.
CC TIGHT junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
CC Repeat; Signal.
CC SIGNAL 1 26 POTENTIAL.
CC CHAIN 27 300 JUNCTIONAL ADHESION MOLECULE 1.
CC DOMAIN 27 238 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 239 259 POTENTIAL.
CC FT DOMAIN 260 299 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 42 115 IG-LIKE V-TYPE DOMAIN 1.
CC FT DOMAIN 145 219 IG-LIKE V-TYPE DOMAIN 2.
CC FT DISULFID 49 108 POTENTIAL.
CC FT DISULFID 152 212 POTENTIAL.
CC FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 300 AA; 32368 MW; 391F3E48FF3B97EC CRC64;
Query Match 11.98; Score 161.5; DB 1; Length 300;
Best Local Similarity 25.58; Pred. No. 2.5e-06;
Matches 65; Conservative 37; Mismatches 108; Indels 45; Gaps 11;
Qy 21 SITPQMIKAKGETAYLPCRTF--LGPEDQGPLDIEWLLSPADNOKVDQVILYSGDK 78
Db 29 SVYTAQSDVQVPENESIKLCTVSGFSSPR-----VEWKV-----QGSTITALVCYN-SQ 77
Qy 79 IYDDYQDLKGRVHFTNDLKGDSINVTNLQLSDIGTYOCKVKKAPG--VGNKKIKQLT 136
Db 78 ITAPY-----ADRVTFSS-----SGITFSSVTRKNGEYTCMVSEGGQNGYGEVSIHLT 126
Qy 137 VLLKPSGTRCVGDSSEIGNDFKLCKPEKGSPLLYEWOK-----LSNSQKLPTLWLA 190
Db 127 VLVPPSPKTTISVSSSVTIGNRAVLTCSEHGDSPSPSEYWFKDGISMLTADAKTRAFMNS 186
Qy 191 EMTSPVLSVKNASTEY-----SGTYSCTVKNRVGSDQCLRLDLVVPVPSNRAGTIAGAV 243

187 SFT---IDPKSGDLIFDPVTFDSGEYCYQAQNGYGT---AMRSEAAHMDAVELNVGGIV 240
244 IGVLLALVLIGLIIF 258
241 AAVLVTLILGLLIF 255

RESULT 8
CD80_MOUSE STANDARD; PRT; 306 AA.
ID CD80_MOUSE
AC Q00609;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1
DE antigen) (B7).
GN CD80 OR B7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91341422; PubMed=1714935;
RA Gray G.S., Freeman G.J., Gimmi C.D., Lombard D.B., Zhou L.J.,
RA White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;
RT "Structure, expression, and T cell costimulatory activity of the
RT murine homologue of the human B lymphocyte activation antigen B7.";
RL J. Exp. Med. 174:625-631(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93307789; PubMed=7686531;
RA Selvakumar A., White P.C., Dupont B.;
RT "Genomic organization of the mouse B-lymphocyte activation antigen
RT B7.";
RL Immunogenetics 38:292-295(1993).
CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA
CC INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL
CC MALIGNANCIES.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-
CC ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND
CC IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC
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CC
CC EMBL: X60958; AAA3291.1; --
CC EMBL: L12589; AAA37240.1; ALT_SEQ.
CC EMBL: L12585; AAA37240.1; JOINED.
CC EMBL: L12586; AAA37240.1; JOINED.
CC EMBL: L12587; AAA37240.1; JOINED.
CC EMBL: L12588; AAA37240.1; JOINED.
CC PIR: S17291; S17291.
CC HSSP; P33681; LDR3.
CC MGD; MGI:101775; Cd80.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR003006; Ig_MHC.

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DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; ig; 2.
DR SMART: SM00409; IG; 1.
DR SMART: SM00410; IG-like; 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL 1 37
FT CHAIN 38 306 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT DOMAIN 38 246 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 247 268
FT DOMAIN 269 306 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 47 126 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 158 226 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 227 246 IG-HINGE LIKE (POTENTIAL).
FT DISULFID 54 119
FT DISULFID 165 219
FT CARBOHYD 93 93 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 99 99 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 306 AA; 34589 MW; 1DBADE0931B84C62 CRC64;

Query Match 11.38; Score 154; DB 1; Length 306;
Best Local Similarity 22.94; Pred. No. 1.e-05;
Matches 65; Conservative 55; Mismatches 108; Indels 56; Gaps 13;

QY 3 LLLCFVLLCGVADLTRSLSTTPTEOMIEKAGETAYLPCTRFTLGPDPQGLDIEWLLSPA 62
Db 21 LILLFVLLIRLSQSSDV-----DEQLSKVKVKKVLLPCRYNPSHEDESDRIYW----- 70
QY 63 DNQKVDQVII-LYSGD-KIYDDYQDLKGRVHFTSNDLKGSDASINVTNLQSLDIGTYQC 120
Db 71 --QKHKVLSVIAKLVKWPVEY--KNRTLYDNTTY-----SLIILGLVLSDRGTYS 119
QY 121 KVKAPGVGNKKQLTLLRPS-----GTRCYVDGSEIENGDFLKPKEGSLPLLYEW 175
Db 120 VVQKKER-GTYEVKHLALVKLSIKADFTSPNITESGNPSADTKRITCFASGFPKPRFSW 178
QY 176 QKLSNSOKLPTLWLAEMTSPVISVKNAST--EYSGTYSCTVKNRVSQDQLRL----- 227
Db 179 --LNGRELPGINTIISQDESELYTISQLDFNTRNHTIK-----CLIKYGDHVS 229
QY 228 -----DVVPPSNRAGTIAGAVIGVLLALVLGLIIFC-CR 261
Db 230 EDFTWKEPPDPDSKNTLVLFAGAGCAVITVVIVIIKCFCK 273

RESULT 9
BUTY BOVIN STANDARD; PRT; 526 AA.
AC P18852; O18955; O18959;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Butyrophilin precursor (BT).
GN BTN1A1 OR BTN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 27-47.
RX MEDLINE=90354441; PubMed=2387867;
RA Jack L.J.W., Mather I.H.;
RT "Cloning and analysis of cDNA encoding bovine butyrophilin, an apical
RT glycoprotein expressed in mammary tissue and secreted in association
RT with the milk-fat globule membrane during lactation.";
RL J. Biol. Chem. 265:14481-14486(1990).
RP [2]
RP SEQUENCE FROM N.A.

STRAIN=Holstein-Friesian;
DAvey H.W., Ogg S.L., Huseini Y., Snell R.G., Korobko I.V.,
MAther I.H., Wilkins R.J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP TISSUE=Blood;
RA Seyfert H., Luethen F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
[4]
RN CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=95293916; PubMed=7775382;
RA Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.;
RL "Site-specific glycosylation of bovine butyrophilin.";
RT J. Biochem. 117:147-157(1995).
CC -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
CC ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; M35551; AAB39766.1; -.
CC EMBL; AF005497; AAB62889.1; -.
CC EMBL; Z93323; CAB07533.1; -.
CC PIR; A37821; A37821.
CC InterPro: IPR001870; Gamma carboxylase.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC InterPro: IPR003878; SPRY domain.
CC InterPro: IPR003877; SPRY_receptor.
CC Pfam; PF00047; ig; 1.
CC Pfam; PF00622; SPRY; 1.
CC SMART; SM00406; IG; 1.
CC SMART; SM00449; SPRY; 1.
KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 26
FT CHAIN 27 526 BUTYROPHILIN.
FT DOMAIN 27 242 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 243 269
FT DOMAIN 270 526 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 55 55 N-LINKED (GLCNAC. .) (COMPLEX).
FT CARBOHYD 215 215 N-LINKED (GLCNAC. .) (HYBRID).
FT CONFLICT 35 35 O -> P (IN REF. 3).
FT CONFLICT 230 230 E -> D (IN REF. 1).
SQ SEQUENCE 526 AA; 59276 MW; A14126802BD19284 CRC64;

Query Match 10.6%; Score 144; DB 1; Length 526;
Best Local Similarity 22.4%; Pred. No. 0.00015;
Matches 63; Conservative 51; Mismatches 121; Indels 46; Gaps 10;

QY 4 LLLCFVLLCGVADLTRSLSTTPTEOMIEKAGETAYLPCTRFTLGPDPQGLDIEWLL---LS 60
Db 13 LLIIFILLPKLSDAPFDVIGQEPILAVVQDAELPCRLSPNVSAKG-MELRWFREKVS 71
QY 61 PADNQKVDQVIIILYSGDKIYDDYQDLKGRVHFTSNDLKGSDASINVTNLQSLDIGTYQC 120
Db 72 PA-----VFVSREGQEQEGEMAEYGRVSLVIEDHIAEGSVAVRIQEVKASDDGEYRC 124
```


FT DISULFID 1594 1610 BY SIMILARITY.
 FT DISULFID 1613 1628 BY SIMILARITY.
 FT DISULFID 1615 1638 BY SIMILARITY.
 FT DISULFID 1641 1650 BY SIMILARITY.
 FT DISULFID 1653 1668 BY SIMILARITY.
 FT DISULFID 1792 1839 BY SIMILARITY.
 FT DISULFID 1886 1932 BY SIMILARITY.
 FT DISULFID 1976 2021 BY SIMILARITY.
 FT DISULFID 2073 2118 BY SIMILARITY.
 FT DISULFID 2170 2215 BY SIMILARITY.
 FT DISULFID 2268 2313 BY SIMILARITY.
 FT DISULFID 2365 2413 BY SIMILARITY.
 FT DISULFID 2456 2506 BY SIMILARITY.
 FT DISULFID 2554 2599 BY SIMILARITY.
 FT DISULFID 2641 2686 BY SIMILARITY.

Query Match 10.08; Score 136.5; DB 1; Length 3707;
 Best Local Similarity 21.39; Pred. No. 0.0069;
 Matches 61; Conservative 38; Mismatches 102; Indels 85; Gaps 12;

QY 20 LSITTPQMEKAGETAYLPCRTGLGPDGGLDIEWLLSPADNQKVDVILYSGDKI 79
 2346 ISIEPSSVQ--QGQASPK---LIHEGAMPIKVEWKI--RDQLEDNVHISPNGSII 2398
 80 -----YDDYY---QDL-----KGRVH-----FTSNDLK 99
 2399 TIVAGPATMEPTACVASNVYGAQSVVNLVSHGPPVSVLPESGPVHVXMGKDITLCEIS 2458
 100 SGD-----ASINVTNLQLSDIGTVCKYKKAAGVGNKK 132
 2459 SGEPRSPRWRTRLGIPVKLEPRMFLMNSHMLKIASVKPSDAGTVYCOAQNALGTAQKQ 2518
 133 IQLTV---LLKPSGTRCYVDGSE---EIGNDFKLCPEKSGSLPLLVEMOKLSNOKLPT 186
 2519 VELIVDTGTVAGPTGPQVQVBESELTLEAGTATLHCS-ATGNPPPTTHWSEK-----RAPL 2573
 187 LWLAEMTSPIVSKVNASTYSGTVCYKRVGSDQCLRLDVVPP 232
 2574 PQHRIEGNTLVIPRAVQDSGGYICNATNSAGHTEATVVLHVESP 2619

RESULT 12
 PVRI HUMAN
 ID PVRI HUMAN STANDARD; PRT; 517 AA.
 AC Q15223; Q75465; Q9HBE6; Q9HBE2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 18-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvEC) (Nectin 1) (Herpesvirus Ig-like receptor) (Higr) (CD111 antigen)
 DE (CD111 antigen)
 GN PVRL1 OR PR1 OR HVEC.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=95237621; PubMed=7721102;
 RA Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C., Dubreuil P.;
 RA "cDNA characterization and chromosomal localization of a gene related to the poliovirus receptor gene.";
 RL Gene 155:261-265(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=98279152; PubMed=9616127;
 RA Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J., Spear P.G.;
 RA "Entry of alphaherpesviruses mediated by poliovirus receptor-related protein 1 and poliovirus receptor.";
 RT Science 280:1618-1620(1998).
 RN [3]

RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
 RX MEDLINE=21256041; PubMed=11356977;
 RA Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J., Campadelli-Fiume G., Dubreuil P.;
 RA "Novel, soluble isoform of the herpes simplex virus (HSV) receptor nectin1 (or pr1-HvEC) modulates positively and negatively RT susceptibility to hsv infection.";
 RL J. Virol. 75:5684-5691(2001).
 RN [4]
 RP SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
 RX MEDLINE=20392396; PubMed=10932188;
 RA Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A., Helms J.A., Spritz R.A.;
 RA "Mutations of PVRL1, encoding a cell-cell adhesion RT molecule/herpesvirus receptor, in cleft lip/palate-ectodermal RT dysplasia.";
 RL Nat. Genet. 25:427-430(2000).
 CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
 CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORMS ALPHA AND DELTA) AND SECRETED (ISOFORM GAMMA).
 CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; ALPHA, DELTA (SHOWN HERE), AND GAMMA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-ectodermal dysplasia syndrome (CLPEDI). It is responsible for allelic forms known as Margarita island form and Zlotogora-Ogur syndrome.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -!- DATABASE: NAME=PROV; NOTE=PROV 2.45-49(2001); WWW="http://www.ncbi.nlm.nih.gov/prov/guide/2005693930_g.htm".
 CC -----
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 CC -----
 CC EMBL: X76400; CAA53980.2; ALT INIT.
 CC EMBL: AF060231; AAC23798.1; -
 CC EMBL: AY029539; AAK33124.1; -
 CC EMBL: AF252867; AAG16648.1; -
 CC EMBL: AF196768; AAG16648.1; JOINED.
 CC EMBL: AF196770; AAG16648.1; JOINED.
 CC EMBL: AF196771; AAG16648.1; JOINED.
 CC EMBL: AF196774; AAG16648.1; -
 CC EMBL: AF196768; AAG16649.1; JOINED.
 CC EMBL: AF196769; AAG16649.1; JOINED.
 CC EMBL: AF196770; AAG16649.1; JOINED.
 CC EMBL: AF196771; AAG16649.1; JOINED.
 CC EMBL: AF196772; AAG16649.1; JOINED.
 CC EMBL: AF196773; AAG16649.1; JOINED.
 CC EMBL: AF196774; AAG16649.1; JOINED.
 CC EMBL: AF196775; AAG16649.1; JOINED.
 CC EMBL: AF196776; AAG16649.1; JOINED.
 CC EMBL: AF196777; AAG16649.1; JOINED.
 CC EMBL: AF196778; AAG16649.1; JOINED.
 CC EMBL: AF196779; AAG16649.1; JOINED.
 CC EMBL: AF196780; AAG16649.1; JOINED.
 CC EMBL: AF196781; AAG16649.1; JOINED.
 CC EMBL: AF196782; AAG16649.1; JOINED.
 CC EMBL: AF196783; AAG16649.1; JOINED.
 CC EMBL: AF196784; AAG16649.1; JOINED.
 CC EMBL: AF196785; AAG16649.1; JOINED.
 CC EMBL: AF196786; AAG16649.1; JOINED.
 CC EMBL: AF196787; AAG16649.1; JOINED.
 CC EMBL: AF196788; AAG16649.1; JOINED.
 CC EMBL: AF196789; AAG16649.1; JOINED.
 CC EMBL: AF196790; AAG16649.1; JOINED.
 CC EMBL: AF196791; AAG16649.1; JOINED.
 CC EMBL: AF196792; AAG16649.1; JOINED.
 CC EMBL: AF196793; AAG16649.1; JOINED.
 CC EMBL: AF196794; AAG16649.1; JOINED.
 CC EMBL: AF196795; AAG16649.1; JOINED.
 CC EMBL: AF196796; AAG16649.1; JOINED.
 CC EMBL: AF196797; AAG16649.1; JOINED.
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FT CHAIN 31 517 POLIOVIRUS RECEPTOR RELATED PROTEIN 1.
FT DOMAIN 31 355 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 356 376 POTENTIAL.
FT DOMAIN 377 517 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 44 131 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 165 233 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 262 323 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 437 444 POLY-GLU.
FT DOMAIN 445 449 POLY-GLY.
FT DISULFID 51 124 BY SIMILARITY.
FT DISULFID 172 226 BY SIMILARITY.
FT DISULFID 269 316 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 335 352 EFTYTPSPHGRAGV -> AFCQLLYPGKGRTRARMF
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FT VARSPLIC 353 517 MISSING (IN ISOFORM GAMMA).
FT VARSPLIC 356 458 FRYTPSPHGRAGVPTALIGVAGSILLVIVGGIV
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Matches 67; Conservative 50; Mismatches 86; Indels 158; Gaps 17;

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DB 44 GTDWLHCSFA-----NPLPSVKITQVTWQKSTNGSKQNVAINPSMGVS 88

QY 79 IYDDYQDLKGRVHTSNDLKSGLASINVTNLQSLDITGYCKKAPGVGNKKIQ--LT 136
DB 89 VLAPY-----RERVEFLRPSFT--DGTIRLSRLEDEGVYICFATFP-TGNRESQNLNT 141

QY 137 VLLKPSCTRCYVDGSEI-----GNDPKL---KCEPKESLPLLYEWOK----- 177
DB 142 VMAKPTN---WISGTONVLRKAGQDDKVLVATCTSANGKPPSVSVSWETRLKGEAYQE 198

QY 178 -----LSNSQKLP-----TLWLAEMTSPVISVKN----- 201
DB 199 RNPNGTWTVISRYRLVPSREAHQOQSLACIVNYHMDRFKESLTNLVQVEPVEVTIEGFG 258

QY 202 -----ASTEY-----SGTYSCTV 214
DB 259 YLQRMVDKLTCKADANPPATEYHTWTLNGLSPKGVQAEQNRTLFFKGPINYSLAGTYICE 318

QY 215 KNRVSGDQCLRLRDV-----PPSN--RAGTIAGAVIG-----VLLALVLGLIIFCC 260
DB 319 TNPIGTRSGQGVNITEFPYTPSPHGRAGVPTALIGGVAGSILLVIVGGIVVAL 378

QY 261 R 261
DB 379 R 379

RESULT 13
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AC Q92078;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

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DE DE Kilon protein precursor (Kindred of IgLON).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_
RP SEQUENCE FROM N.A., AND SEQUENCE OF 32-62.
RX MEDLINE=99175207; PubMed=10075727;
RA Funatsu N., Miyata S., Kumanogoh H., Shigeta M., Hamada K., Endo Y.,
RA Sokawa Y., Maekawa S.;
RT "Characterization of a novel rat brain glycosylphosphatidylinositol-
RT anchored protein (Kilon), a member of the IgLON cell adhesion molecule
RT family.";
RT J. Biol. Chem. 274:8224-8230(1999).
RL CC -!- FUNCTION: CELL-ADHESION (POTENTIAL).
CC CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
CC CC -!- PTM: GLYCOSYLATED.
CC CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. IGLON
CC SUBFAMILY.
CC CC -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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DR EMBL; AB017139; BAA75649.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003600; IG_Like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00408; IGC2; 2.
DR Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal.
FT SIGNAL 1 31
FT CHAIN 32 348 KILON PROTEIN.
FT PROPEP ? 348 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 47 119 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 147 204 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 232 298 IG-LIKE C2-TYPE DOMAIN 3.
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FT DISULFID 239 291 POTENTIAL.
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
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Query Match 9.7%; Score 131.5; DB 1; Length 348;
Best Local Similarity 21.3%; Pred. No. 0.00096;
Matches 74; Conservative 39; Mismatches 114; Indels 121; Gaps 14;

QY 5 LCFVLLCGVADLRSLSTTPPEQMIK---ARKETAYLPCRFTLGPEDQGLDIEWLLSP 61
DB 15 LAAVLLSLCCLPAGQSVDFPWAADVNDMLVRKGDATVLRCLY-----EDGASKGAMLNRS 69

QY 62 ADNQKVDQVILYSGDKIYDDYQDLKGRVHTSNDLKSGLASINVTNLQSLDITGYCK 121
DB 70 S-----IIFAGDK-----WSVDPKVSIST--LNKRYSLOIQNVDTVDGSPYTC 113

QY 122 VKKAPGVGNKTKQLTVLLKP-----SGTR---C----- 146
DB 114 VQHTQFTRTMQVHLTVQVPPKIVISNDMTINEGNTVTLTCLATGKPEPAISWRHGPSA 173

QY 147 -----YVD-----GSEIGN 156

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Db 174 KPENGQYLDIYGTTRDQAGEYECSEAENDVSFPDVKVVRVNVNFAPTIQBIKSGTVPGR 233
Qy 157 DFLLKCEPKESPLLYEWOK---LSNSQKLTMLAEMTSPVISVKNASTYSYSGTISC 212
Db 234 SGLIRCE-GAGVPPAPAFYKBEKLFNGQO-GIIIONFSTKILTVNTQBHFGNYTC 291
Qy 213 TVNRRVSGDQCLRLDVPVPSNRAGTIAGAVIGVL---LALVLIGLI 256
Db 292 VAANKLGTWASPLN--PPSTAQYGITGSACDLFSCWSLALTSSVI 337

RESULT 14
PVRL_PIG ID PVRL_PIG STANDARD; PRT; 515 AA.
AC QGL76;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (HvEC) (Nectin 1).
GN PVRL1 OR PRRI OR HVEC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001).
CC -1- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
CC ALPHAPERPEVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
CC CELLS.
CC -1- SUBUNIT: Interacts with HSV glycoprotein D (gpD) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF308632; AAG30281.1; .
CC HSPSP; P06907; INEU.
CC DR InterPro; IPR003599; Ig.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR InterPro; IPR003598; Ig_c2.
CC DR InterPro; IPR003600; Ig_like.
CC DR InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00409; IG; 3.
CC SMART; SM00410; IG like; 1.
CC SMART; SM00408; IGc2; 2.
CC SMART; SM00406; IGv; 1.
CC Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
KW Repeat; Glycoprotein; Signal.
KW SIGNAL 1 30
FT CHAIN 31 515 POLIOVIRUS RECEPTOR RELATED PROTEIN 1.
FT DOMAIN 31 355 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 356 376 POTENTIAL.
FT DOMAIN 377 515 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 44 131 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 165 233 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 262 323 IG-LIKE C2-TYPE DOMAIN 2.
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FT DOMAIN 437 443 POLY-GLU.
FT DOMAIN 444 447 POLY-GLY.
FT DISULFID 51 124 BY SIMILARITY.
FT DISULFID 172 226 BY SIMILARITY.
FT DISULFID 269 316 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 515 AA; 57047 MW; BFAB00320DDE3785 CRC64;

Query Match 9.5%; Score 129.5; DB 1; Length 515;
Best Local Similarity 18.5%; Pred. No. 0.0023;
Matches 67; Conservative 50; Mismatches 86; Indels 159; Gaps 18;

Qy 34 GETAYLPCTRFTLGPEDQGLDIWLLSPADNOKVDQV-----IILYS---GDK 78
Db 44 GTDVLHCSFA-----NPLPGVKITQVTWQKATNGSKQNVAINPAMGVS 88
Qy 79 IYDDYYQDLKGRVHFTSNDLKSGDASINVTNQLSDIGTYQCKVKKAPGVNKKIQ--LT 136
Db 89 VLAPY---RERVEFLRPSFT--DGTIRLSRLEDEGVVYCFATFP--AGNRESQNLNT 141
Qy 137 VLLKPSGTRCYVDGSEEI-----GNDFKL---KCEPKESLPLLYEWOK----- 177
Db 142 VMAKPTN--WIEGTQAVLRKAKDKDKVLVATCTSANGKPPSVSVSWETHLKGEAEYQEI 198
Qy 178 -----LSNSQKLP-----TLMAEMTSPVISVKN----- 201
Db 199 RNPNGTIVTISRYLVPSREDHRHQSLACIVNHNDRFESLTINVQYEVETIEGFGNW 258
Qy 202 -----ASTEY-----SGTYSCTV 214
Db 259 YLQDMVDKLTCKADANPPATEYHWTTLNGLSLPKGVEAQNRTLFFRGPINYSMACTVCEA 318
Qy 215 KNRVSGDQCLRLDQV-----PPSN--RAGTIAGAVIG-----VLLALVLI-GLIIFC 259
Db 319 TNPITRSGQVEVNITEFTPTSPPEHRRAGQVPTAIIGGVVGSILLVLFVVGGIIVAL 378
Qy 260 CR 261
Db 379 CR 380

RESULT 15
PGEM_HUMAN STANDARD; PRT; 4393 AA.
ID PGEM_HUMAN STANDARD; PRT; 4393 AA.
AC P98160; Q16287;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Basement membrane-specific heparan sulfate proteoglycan core
DE protein precursor (HSPG) (Perlecan) (PLC).
GN HSPG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92112994; PubMed=1730768;
RA Kallunki P., Tryggvason K.;
RT "Human basement membrane heparan sulfate proteoglycan core protein: a
RT 467-kD protein containing multiple domains resembling elements of the
RT low density lipoprotein receptor, laminin, neural cell adhesion
RT molecules, and epidermal growth factor.";
RL J. Cell Biol. 116:559-571(1992).
RN [2]
RP SEQUENCE FROM N.A.
```

RC TISSUE=Skin, and Colon;
RX MEDLINE=92235084; PubMed=1569102;
RA Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;
RT "Primary structure of the human heparan sulfate proteoglycan from
basement membrane (HSPG2/perlecan). A chimeric molecule with multiple
domains homologous to the low density lipoprotein receptor, laminin,
RT neural cell adhesion molecules, and epidermal growth factor.";
RL J. Biol. Chem. 267:8544-8557(1992).
RN [3]
RP SEQUENCE OF 1018-1472 FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=91365376; PubMed=1679749;
RA Dodge G.R., Kovalesky I., Chu M.L., Hassell J.R., McBride O.W.,
RA Yi H.F., Iozzo R.V.;
RT "Heparan sulfate proteoglycan of human colon: partial molecular
cloning, cellular expression, and mapping of the gene (HSPG2) to the
RT short arm of human chromosome 1.";
RL Genomics 10:673-680(1991).
RN [4]
RP SEQUENCE OF 892-1398 FROM N.A.
RC TISSUE=Fibrosarcoma;
RX MEDLINE=92120660; PubMed=1685141;
RA Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,
RA Trygvaeson K.;
RT "Cloning of human heparan sulfate proteoglycan core protein,
RT assignment of the gene (HSPG2) to 1p36.1--p35 and identification of
RT a BamHI restriction fragment length polymorphism.";
RL Genomics 11:389-396(1991).
RN [5]
RP SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=94052171; PubMed=8234307;
RA Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.;
RT "Structural characterization of the complete human perlecan gene and
RT its promoter.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).
CC -!- FUNCTION: This protein is an integral component of basement
membranes. It is responsible for the fixed negative electrostatic
charge and is involved in the charge-selective ultrafiltration
properties. It serves as an attachment substrate for cells.
CC -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in
dimers or stellate structures. It interacts with other basement
membrane components such as laminin, prolargin and collagen type
IV.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.
CC -!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED
AND O-LINKED OLIGOSACCHARIDES.
CC -!- SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.
CC -!- SIMILARITY: CONTAINS 10.5 LAMININ EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 LAMININ DOMAINS IV.
CC -!- SIMILARITY: CONTAINS 22 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 SEA DOMAIN.
CC -----
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CC -----
DR EMBL; X62515; CAA44373.1; --
DR EMBL; M85289; AAA52700.1; --
DR EMBL; M64283; AAA52699.1; --
DR EMBL; S76436; AAB21121.2; --
DR EMBL; L22078; -; NOT_ANNOTATED_CDS.
DR HSSP; P00740; 1EDM.
DR SienA-2DPAGE; P98160; --
DR Genew; HGNC:5273; HSPG2.
DR MIM; 142461; --
DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR002172; LDL_recept_A.
DR InterPro; IPR000034; Laminin_B_-.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR000082; SEA_domain.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00047; ig; 22.
DR Pfam; PF00052; laminin_B; 3.
DR Pfam; PF00053; laminin_EGF; 7.
DR Pfam; PF00054; laminin_G; 3.
DR Pfam; PF00057; ldl_recept_a; 4.
DR Pfam; PF01390; SEA; 1.
DR PRINTS; PR00010; EGFBL00D.
DR ProDom; PD003031; Laminin_B; 3.
DR SMART; SM00180; EGF_Lam; 6.
DR SMART; SM00001; EGF_like; 8.
DR SMART; SM00408; IGC2; 22.
DR SMART; SM00192; LDLa; 4.
DR SMART; SM00281; LamB; 3.
DR SMART; SM00282; LamG; 3.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS01248; LAMININ TYPE EGF; 11.
DR PROSITE; PS00025; LAM G DOMAIN; 3.
DR PROSITE; PS01309; LDLRA_1; 4.
DR PROSITE; PS00668; LDLRA_2; 4.
DR PROSITE; PS50024; SEA; 1.
DR Signal; Basement membrane; Proteoglycan; Repeat; Glycoprotein;
KW Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;
KW Extracellular matrix; EGF-like domain.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 4393 BASEMENT MEMBRANE-SPECIFIC HEPARAN
SULFATE PROTEOGLYCAN CORE PROTEIN.
FT DOMAIN 80 194 SEA.
FT DOMAIN 197 236 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 283 321 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 323 361 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 366 405 LDL-RECEPTOR CLASS A 4.
FT DOMAIN 405 506 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 523 532 LAMININ EGF-LIKE 1 (N-TERMINAL).
FT DOMAIN 533 732 LAMININ DOMAIN IV 1 (DOMAIN III A).
FT DOMAIN 733 765 LAMININ EGF-LIKE 1 (C-TERMINAL).
FT DOMAIN 766 815 LAMININ EGF-LIKE 2.
FT DOMAIN 816 873 LAMININ EGF-LIKE 3.
FT DOMAIN 881 925 LAMININ EGF-LIKE 4 (INCOMPLETE).
FT DOMAIN 926 935 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 936 1127 LAMININ DOMAIN IV 2 (DOMAIN III B).
FT DOMAIN 1128 1160 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 1161 1210 LAMININ EGF-LIKE 6.
FT DOMAIN 1211 1267 LAMININ EGF-LIKE 7.
FT DOMAIN 1277 1326 LAMININ EGF-LIKE 8.
FT DOMAIN 1327 1336 LAMININ EGF-LIKE 9 (N-TERMINAL).
FT DOMAIN 1337 1531 LAMININ DOMAIN IV 3 (DOMAIN III C).
FT DOMAIN 1532 1564 LAMININ EGF-LIKE 9 (C-TERMINAL).
FT DOMAIN 1565 1614 LAMININ EGF-LIKE 10.
FT DOMAIN 1615 1672 LAMININ EGF-LIKE 11.
FT DOMAIN 1679 1773 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 1774 1867 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 1868 1957 IG-LIKE C2-TYPE DOMAIN 4.
FT DOMAIN 1958 2053 IG-LIKE C2-TYPE DOMAIN 5.
FT DOMAIN 2054 2153 IG-LIKE C2-TYPE DOMAIN 6.
FT DOMAIN 2154 2246 IG-LIKE C2-TYPE DOMAIN 7.
FT DOMAIN 2247 2342 IG-LIKE C2-TYPE DOMAIN 8.
FT DOMAIN 2343 2438 IG-LIKE C2-TYPE DOMAIN 9.
FT DOMAIN 2439 2535 IG-LIKE C2-TYPE DOMAIN 10.
FT DOMAIN 2536 2631 IG-LIKE C2-TYPE DOMAIN 11.
FT DOMAIN 2632 2728 IG-LIKE C2-TYPE DOMAIN 12.
FT DOMAIN 2729 2828 IG-LIKE C2-TYPE DOMAIN 13.

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FT DOMAIN 2829 2926 IG-LIKE C2-TYPE DOMAIN 14.
FT DOMAIN 2927 3023 IG-LIKE C2-TYPE DOMAIN 15.
FT DOMAIN 3024 3114 IG-LIKE C2-TYPE DOMAIN 16.
FT DOMAIN 3115 3213 IG-LIKE C2-TYPE DOMAIN 17.
FT DOMAIN 3214 3300 IG-LIKE C2-TYPE DOMAIN 18.
FT DOMAIN 3301 3401 IG-LIKE C2-TYPE DOMAIN 19.
FT DOMAIN 3402 3490 IG-LIKE C2-TYPE DOMAIN 20.
FT DOMAIN 3491 3576 IG-LIKE C2-TYPE DOMAIN 21.
FT DOMAIN 3577 3664 IG-LIKE C2-TYPE DOMAIN 22.
FT DOMAIN 3665 3845 LAMININ G-LIKE 1.
FT DOMAIN 3846 3883 EGF-LIKE 1.
FT DOMAIN 3886 3924 EGF-LIKE 2.
FT DOMAIN 3930 4105 LAMININ G-LIKE 2.
FT DOMAIN 4106 4143 EGF-LIKE 3.
FT DOMAIN 4145 4178 EGF-LIKE 4.
FT DOMAIN 4203 4391 LAMININ G-LIKE 3.
FT SITE 65 67 HEPARAN SULFATE (POTENTIAL).
FT SITE 71 73 HEPARAN SULFATE (POTENTIAL).
FT SITE 76 78 HEPARAN SULFATE (POTENTIAL).
FT SITE 4151 4153 MEDIATES MOTOR NEURON ATTACHMENT
(POTENTIAL).
FT SITE 4301 4303 MEDIATES MOTOR NEURON ATTACHMENT
(POTENTIAL).
FT DISULFID 199 212 BY SIMILARITY.
FT DISULFID 206 225 BY SIMILARITY.
FT DISULFID 219 234 BY SIMILARITY.
FT DISULFID 285 297 BY SIMILARITY.
FT DISULFID 292 310 BY SIMILARITY.
FT DISULFID 304 319 BY SIMILARITY.
FT DISULFID 325 337 BY SIMILARITY.
FT DISULFID 332 350 BY SIMILARITY.

Query Match 9.58; Score 128.5; DB 1; Length 4393;
Best Local Similarity 23.3%; Pred. No. 0.04;
Matches 50; Conservative 35; Mismatches 75; Indels 55; Gaps 11;

Qy 20 LSITTPQMIKAGETAYLPCRFTLGPEDQGLDIEWLLSPADNOKVDQVILYSGDKI 79
Db 3026 ISIDPPSSVQ--QGQDASFKC---LIHDGAAPISLEW----- 3058
Qy 80 YDDYYQDLKGRVHTSNDLKGDSASINVTNLQLSIDCTYQCKVKAPGVGNKKIQL---- 135
Db 3059 -KTRNQELEDNVHISPN-----GSIITVGTSPSNHCTRCVASNAYGVAQSVVNLVSHG 3112
Qy 136 --TVLLKPSGTRCYVDSGEIGNDFLKC----EPKEGSLPLLYEWQKLSNS-QKLP TLW 188
Db 3113 PPTVSVLPEGP-VWV-----KVGKAVTLECVSAGEPRSSA-----RWTRISSTPAKLEQRT 3162
Qy 189 LAEMTS-PVISVKNASTEYSGTYSCTVKNRVGSDQ 222
Db 3163 YGLMDSHTVLIQISSAKPSDAGTVVCLAQNALGTAQ 3197

```

Search completed: July 9, 2003, 12:44:49
Job time : 11 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 12:42:53 ; Search time 32 Seconds
(without alignments)
1680.572 Million cell updates/sec

Title: US-09-899-634C-2

Perfect score: 1359

Sequence: 1 MALLLCFVLLCGVADLTRSL.....AVIGVLLVLLGLIIFCCR 261

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL 21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1341	98.7	319	6	Q9TU79	Q9tu79 sus scrofa
2	1270	93.5	365	6	Q8WV3	Q8wmv3 bos taurus
3	1254	92.3	319	6	Q9TU80	Q9tu80 canis famil
4	1238	91.1	344	4	Q9UKV4	Q9ukv4 homo sapien
5	1233	90.7	344	11	Q9R067	Q9r067 rattus norv
6	1233	90.7	358	11	Q9R066	Q9r066 rattus norv
7	1216	89.5	352	11	Q9R066	Q9r066 mus musculu
8	1216	89.5	366	11	Q9R066	Q9r066 mus musculu
9	921	67.8	252	4	Q8WWT6	Q8wwt6 homo sapien
10	676	49.7	200	4	Q8WWT7	Q8wwt7 homo sapien
11	659.5	48.5	372	13	Q9YV50	Q9y50 brachydanio
12	641	47.2	164	11	Q9YV50	Q9y50 mus musculu
13	378.5	27.9	373	4	Q9H6B4	Q9hb64 homo sapien
14	366.5	27.0	373	11	Q8R373	Q8r373 mus musculu
15	362.5	26.7	373	11	Q920S5	Q920s5 mus musculu
16	338	24.9	89	4	Q8WWT8	Q8wwt8 homo sapien

17	321.5	23.7	319	11	Q922D5	Q922d5 mus musculu
18	311.5	22.9	319	11	Q9UKA5	Q9uk5 mus musculu
19	301	22.1	284	4	Q9NX42	Q9nx42 homo sapien
20	301	22.1	327	4	Q96IQ7	Q96iq7 homo sapien
21	297	21.9	304	11	Q9CVA4	Q9cva4 mus musculu
22	295	21.7	325	4	Q9S791	Q9s791 homo sapien
23	291	21.4	318	13	Q91664	Q91664 xenopus lae
24	289	21.3	328	11	Q92109	Q92109 mus musculu
25	282	20.8	335	13	Q9YGV5	Q9ygv5 gallus gall
26	276	20.3	335	13	Q9PWR4	Q9pwr4 gallus gall
27	273	20.1	335	13	Q9YGH1	Q9ygh1 gallus gall
28	255	18.8	407	11	Q9D2J4	Q9d2j4 mus musculu
29	254	18.7	248	11	Q9D0T4	Q9d0t4 mus musculu
30	250	18.4	259	4	Q9S532	Q9s532 homo sapien
31	246.5	18.1	394	11	Q925F2	Q925f2 mus musculu
32	226	16.6	390	6	Q95KI3	Q95ki3 macaca fasc
33	217	16.0	390	4	Q96T50	Q96t50 homo sapien
34	217	16.0	390	4	Q96AP7	Q96ap7 homo sapien
35	195.5	14.4	181	13	Q91665	Q91665 xenopus lae
36	188.5	13.9	300	11	Q9D9J0	Q9d9j0 mus musculu
37	187.5	13.8	300	11	Q9DA22	Q9da22 mus musculu
38	175.5	12.9	300	11	Q9JHY1	Q9jhy1 rattus norv
39	171.5	12.6	298	11	Q9J159	Q9j159 mus musculu
40	169	12.4	280	13	Q9J716	Q9j716 grus americ
41	165	12.1	259	4	Q9Y5B2	Q9y5b2 homo sapien
42	163.5	12.0	399	4	Q9Y279	Q9y279 homo sapien
43	161.5	11.9	300	11	Q8VC39	Q8vc39 mus musculu
44	159.5	11.7	4162	13	Q98918	Q98918 gallus gall
45	159	11.7	5198	5	Q76518	Q76518 caenorhabdi

ALIGNMENTS

RESULT 1

Q9TU79 PRELIMINARY; PRT; 319 AA.

AC Q9TU79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cxsackie-adenovirus-receptor homolog (Fragment).
GN CAR.

OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RX MEDLINE=99422053; PubMed=10490761;

RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,

RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultheiss H.-P.,

RA Lamers J.M.J., Poller W.;

RT "Expression of Cxsackie-adenovirus-receptor and alpha v-integrin does

RT not correlate with adenovector targeting in vivo indicating anatomical

RT vector barriers."

RL Gene Ther. 6:1520-1535(1999).

DR EMBL; AF109646; AAF01257.1; -.

DR InterPro; IPR003598; Ig_c2.

DR InterPro; IPR003600; Ig_like.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00408; IGC2; 1.

DR SMART; SM00410; IG_like; 1.

DR Immunoglobulin domain; Receptor.

FT NON TER 319

SQ SEQUENCE 319 AA; 35301 MW; C485555A6C9F1B5B CRC64;

Query Match 98.7%; Score 1341; DB 6; Length 319;

Best Local Similarity 99.2%; Pred. No. 3.2e-112;

Matches 258; Conservative 1; Mismatches 1; Indels 0; Gaps 0;


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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang X., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultzeiss H.-P.,
RA Lamers J.M.J., Poller W.;
RT "Expression of Coxackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers."
RL Gene Ther. 6:1520-1535 (1999).
DR EMBL; AF109643; AAF01254.1; -.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG like; 1.
KW Immunoglobulin domain; Receptor.
FT NON_TER 344 344
SQ SEQUENCE 344 AA; 38097 MW; BEF3722E96C697AA CRC64;

Query Match 91.1%; Score 1238; DB 4; Length 344;
Best Local Similarity 89.3%; Pred. No. 6.4e-103;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTRSLITTPPEOMIEKAGETAYLPCRTFLGPDGQPLDIEWLLS 60
DB 1 MALLLCFVLLCGVADLTRSLITTPPEOMIEKAGETAYLPCRTFLGPDGQPLDIEWLLS 60
QY 61 PADNOKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIGTYQC 120
DB 61 PADNOKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIGTYQC 120
QY 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEBEIGNDFKLCPEKESLPLLYEWQKLSN 180
DB 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEBEIGNDFKLCPEKESLPLLYEWQKLSN 180
QY 181 SOKLPTLWLAEMTSPVISVKNASSTGYCTVKNRVSQDCLLRDLVVPPSNRAGTIA 240
DB 181 SOKMPTSLWLAEMTSPVISVKNASSTGYCTVKNRVSQDCLLRDLVVPPSNRAGTIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 5
QY067 ID QY067 PRELIMINARY; PRT; 344 AA.
AC QY067;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Coxackie-adenovirus-receptor homolog (Fragment).
GN CAR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=LIVER;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultzeiss H.-P.,
RA Lamers J.M.J., Poller W.;
RT "Expression of Coxackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers."
RL Gene Ther. 6:1520-1535 (1999).
DR EMBL; AF109644; AAF01255.1; -.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG like; 1.
KW Immunoglobulin domain; Receptor.
FT NON_TER 358 358
SQ SEQUENCE 358 AA; 39261 MW; 731B7384A786BB04 CRC64;
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RT vector barriers."
RL Gene Ther. 6:1520-1535 (1999).
DR EMBL; AF109643; AAF01254.1; -.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG like; 1.
KW Immunoglobulin domain; Receptor.
FT NON_TER 344 344
SQ SEQUENCE 344 AA; 38030 MW; D436498820D8B9B7 CRC64;

Query Match 90.7%; Score 1233; DB 11; Length 344;
Best Local Similarity 89.6%; Pred. No. 1.8e-102;
Matches 233; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTRSLITTPPEOMIEKAGETAYLPCRTFLGPDGQPLDIEWLLS 60
DB 1 MALLLCFVLLCGVADLTRSLITTPPEOMIEKAGETAYLPCRTFLGPDGQPLDIEWLLS 60
QY 61 PADNOKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIGTYQC 120
DB 61 PADNOKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIGTYQC 120
QY 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEBEIGNDFKLCPEKESLPLLYEWQKLSN 180
DB 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEBEIGNDFKLCPEKESLPLLYEWQKLSN 180
QY 181 SOKLPTLWLAEMTSPVISVKNASSTGYCTVKNRVSQDCLLRDLVVPPSNRAGTIA 240
DB 181 SOKMPTSLWLAEMTSPVISVKNASSTGYCTVKNRVSQDCLLRDLVVPPSNRAGTIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 260
DB 241 GAVIGVLLALVLIIGLIIFCCR 260

RESULT 6
QY066 ID QY066 PRELIMINARY; PRT; 358 AA.
AC QY066;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Coxackie-adenovirus-receptor homolog (Fragment).
GN CAR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=LIVER;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultzeiss H.-P.,
RA Lamers J.M.J., Poller W.;
RT "Expression of Coxackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers."
RL Gene Ther. 6:1520-1535 (1999).
DR EMBL; AF109644; AAF01255.1; -.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG like; 1.
KW Immunoglobulin domain; Receptor.
FT NON_TER 358 358
SQ SEQUENCE 358 AA; 39261 MW; 731B7384A786BB04 CRC64;
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Query Match      90.7%; Score 1233; DB 11; Length 358;
Best Local Similarity 89.6%; Pred. No. 1.9e-102;
Matches 233; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTRSLITTPQMIKAKGETAYLPCRTLTGDPDQGLDIEWLLS 60
DB 1 MALLLCFVLLCGVADFTSLITTPQRIEKAKGETAYLPCRTLTGDPDQGLDIEWLLS 60

QY 61 PADNOKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIGTYQC 120
DB 61 PSDNQIVDQVILYSGDKIYDNYYPDLKGRVHFTSNDVKS GDASINVTNLQLSDIGTYQC 120

QY 121 KVKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFKLKCPKSGSLPLLVEWOKLSN 180
DB 121 KVKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFKLKCPKSGSLPLLVEWOKLSN 180

QY 181 SOKLPTLWLAEMTSPVISVKNASTEYSGTYSCTVKNRVGSDQCLLRDLVVPSPNRAGTIA 240
DB 181 SOKLPTLWLAEMTSPVISVKNASTEYSGTYSCTVKNRVGSDQCLLRDLVVPSPNRAGTIA 240

QY 241 GAVIGVLLALVLGLIIFCC 260
DB 241 GAVIGVLLALVLGLIIFCC 260

RESULT 7
ID Q91W66 PRELIMINARY; PRT; 352 AA.
AC Q91W66;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Cxsackievirus and adenovirus receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LIVER;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fuhunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
DR EMBL; AK004908; BAB23660.1; -.
DR MGD; MGI:1201679; Cxadr.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00410; IG_like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 352 AA; 38843 MW; 2BD8CBD25D8CE123 CRC64;

Query Match      89.5%; Score 1216; DB 11; Length 352;
Best Local Similarity 88.1%; Pred. No. 6.3e-101;
Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTRSLITTPQMIKAKGETAYLPCRTLTGDPDQGLDIEWLLS 60
DB 1 MALLLCFVLLCGVADFTSLITTPQRIEKAKGETAYLPCRTLTGDPDQGLDIEWLLS 60

QY 61 PADNOKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIGTYQC 120
DB 61 PSDNQIVDQVILYSGDKIYDNYYPDLKGRVHFTSNDVKS GDASINVTNLQLSDIGTYQC 120

QY 121 KVKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFKLKCPKSGSLPLLVEWOKLSN 180
DB 121 KVKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFKLKCPKSGSLPLLVEWOKLSN 180

QY 181 SOKLPTLWLAEMTSPVISVKNASTEYSGTYSCTVKNRVGSDQCLLRDLVVPSPNRAGTIA 240
DB 181 SOKLPTLWLAEMTSPVISVKNASTEYSGTYSCTVKNRVGSDQCLLRDLVVPSPNRAGTIA 240

QY 241 GAVIGVLLALVLGLIIFCC 260
DB 241 GAVIGVLLALVLGLIIFCC 260
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RESULT 8
ID Q9DBJ8 PRELIMINARY; PRT; 366 AA.
AC Q9DBJ8;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Cxsackievirus and adenovirus receptor.
GN CXADR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LIVER;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fuhunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
DR EMBL; AK004908; BAB23660.1; -.
DR MGD; MGI:1201679; Cxadr.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00410; IG_like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 366 AA; 40078 MW; D1C3CA7163F3B231 CRC64;

Query Match      89.5%; Score 1216; DB 11; Length 366;
Best Local Similarity 88.1%; Pred. No. 6.6e-101;
Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTRSLITTPQMIKAKGETAYLPCRTLTGDPDQGLDIEWLLS 60
DB 1 MALLLCFVLLCGVADFTSLITTPQRIEKAKGETAYLPCRTLTGDPDQGLDIEWLLS 60

QY 61 PADNOKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIGTYQC 120
DB 61 PSDNQIVDQVILYSGDKIYDNYYPDLKGRVHFTSNDVKS GDASINVTNLQLSDIGTYQC 120

QY 121 KVKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFKLKCPKSGSLPLLVEWOKLSN 180
DB 121 KVKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFKLKCPKSGSLPLLVEWOKLSN 180

QY 181 SOKLPTLWLAEMTSPVISVKNASTEYSGTYSCTVKNRVGSDQCLLRDLVVPSPNRAGTIA 240
DB 181 SOKLPTLWLAEMTSPVISVKNASTEYSGTYSCTVKNRVGSDQCLLRDLVVPSPNRAGTIA 240

QY 241 GAVIGVLLALVLGLIIFCC 260
DB 241 GAVIGVLLALVLGLIIFCC 260
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RESULT 9
Q8WWT6 PRELIMINARY; PRT; 252 AA.
AC Q8WWT6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cocksackie-adenovirus-receptor isoform CAR4/7.
CXADR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dornier A., Xiong D., Yajima T., Knowlton K.U.;
RT "A soluble coxsackie adenovirus receptor is elevated in Cocksackie B3
RT infected mice.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY072912; AAL68880.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003600; IG_like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_like; 1.
KW Receptor.
SQ SEQUENCE 252 AA; 28201 MW; 4532559D01AB67E2 CRC64;

Query Match 67.8%; Score 921; DB 4; Length 252;
Best Local Similarity 83.4%; Pred. No. 1.2e-74;
Matches 176; Conservative 8; Mismatches 13; Indels 14; Gaps 1;

QY 1 MALLLCFVLLCGVADLTRSLITTPQMIKAKGETAYLPCRFTLGPEDQGPLDIEWLLS 60
DB 1 MALLLCFVLLCGVVDVFARSLSITTPQMIKAKGETAYLPCRFTLGPEDQGPLDIEWLLS 60

QY 61 PADNQKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIGTYQC 120
DB 61 PADNQKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIGTYQC 120

QY 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIEGNDFKLKPCKEKSPLLYEW 180
DB 121 KVKKAPGVGNKKIHLVVLVPRSGARCVDGSEIEGSDFKIKCPKESLPLQYEWOKLSD 180

QY 181 SOKLPTLWLA-----EMTSPVI 197
DB 181 SQKMTSWLAGKWKCHLQRAVRPLPEATSAVI 211

RESULT 10
Q8WWT7 PRELIMINARY; PRT; 200 AA.
AC Q8WWT7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cocksackie-adenovirus-receptor isoform CAR3/7.
CXADR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dornier A., Xiong D., Yajima T., Knowlton K.U.;
RT "A soluble coxsackie adenovirus receptor is elevated in Cocksackie B3
RT infected mice.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY072911; AAL68879.1; -.
DR InterPro; IPR003599; IG.
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DR InterPro; IPR003600; IG_like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_like; 1.
KW Receptor.
SQ SEQUENCE 200 AA; 22370 MW; 43FDB19DF6A7FEB8 CRC64;

Query Match 49.7%; Score 676; DB 4; Length 200;
Best Local Similarity 75.4%; Pred. No. 8.8e-53;
Matches 132; Conservative 12; Mismatches 19; Indels 12; Gaps 2;

QY 1 MALLLCFVLLCGVADLTRSLITTPQMIKAKGETAYLPCRFTLGPEDQGPLDIEWLLS 60
DB 1 MALLLCFVLLCGVVDVFARSLSITTPQMIKAKGETAYLPCRFTLGPEDQGPLDIEWLLS 60

QY 61 PADNQKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIGTYQC 120
DB 61 PADNQKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIGTYQC 120

QY 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIEGNDFKLKPCKEKSPLLYEW 175
DB 121 KVKKAPGVGNKKIHLVVLVPRSGARCVDGSEIEGNDFKLKPCKEKSPLLYEW 163

RESULT 11
Q90Y50 PRELIMINARY; PRT; 372 AA.
AC Q90Y50;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cocksackie virus and adenovirus receptor-like protein.
GN CAR.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20535037; PubMed=11080637;
RA van Raaij M.J., Chouin E., van der Zandt H., Bergelson J.M.,
RA Cusack S.;
RT "Dimeric structure of the coxsackievirus and adenovirus receptor D1
RT domain at 1.7 A resolution.";
RL Structure 8:1147-1155(2000).
DR EMBL; AF268197; AAKS8592.1; -.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 2.
KW Receptor.
SQ SEQUENCE 372 AA; 40664 MW; C363B71E7601C73A CRC64;

Query Match 48.5%; Score 659.5; DB 13; Length 372;
Best Local Similarity 45.8%; Pred. No. 6.5e-51;
Matches 121; Conservative 57; Mismatches 73; Indels 13; Gaps 3;

QY 3 LLLCFVLL-----CGVADLTRSLIT-TPEQMIKAKGETAYLPCRFTLGPEDQGPLDIE 56
DB 8 LCYVYVILLTGSACG-----LQITSTGQTSIEKASGESVKLDCQFTLASDDSGPLDIE 60

QY 57 WLLSPADNOKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIG 116
DB 61 WSLQPSDNQKEKQVIVYSGDRAFEHYDPLKGRVHFNPSDPKNGDASNNMGLKATDITG 120

QY 117 TYQCKVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIEGNDFKLKPCKEKSPLLYEW 176
DB 121 TYQCKIKVPGIARSKYLLTVNVPSPKPKCSAEGQTYVGKNMVLKCSSVEGTQPMYIWE 180

QY 177 KLSNOKPLTLAEMTSPVIVSKVASTSYGTSCTVKNRYSVGSODCLRLDQVPPSNRA 236
DB 181 RTSGNKLPLPLAILDKVTGTMTLKNATGASGYRCQAKNRVGTGECVVEVITTPQNTA 240
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QY 237 GTIAGAVIGVLLALVLIHGLIIFCC 260
Db 241 GTIAGVILCILLALLLALLIIFCC 264

RESULT 12
ID Q99KGO PRELIMINARY; PRT; 164 AA.
AC Q99KGO;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to coxsackievirus and adenovirus receptors.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004680; AA04680.1; -.
DR HSSP; P33681; IDR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
KW Receptor.
SQ SEQUENCE 164 AA; 17781 MW; 9DFPCBD456240C73 CRC64;

Query Match 47.2%; Score 641; DB 11; Length 164;
Best Local Similarity 86.6%; Pred. No. 9.3e-50;
Matches 123; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 MALLCFVLCCGVADLTRSLITTPQMIKAKGETAYLPCRTFLGPDQGLDIEWLIS 60
Db 1 MARLLCFVLCCGIADFTSGLSITTPQRIEAKAKGETAYLPCRTFLGPDQGLDIEWLIS 60

QY 61 PADNOKVDQVILYSGDKIYDDYODLKGKVHFTSNDLKSGLASINVTNLQSLDICTYQC 120
Db 61 PSDNQIVDQVILYSGDKIYDNYDPLDKGRVHFTSNDVKSGLASINVTNLQSLDICTYQC 120

QY 121 KVKKAPGVGNKKIQLTVLLKPS 142
Db 121 KVKKAPGVANKKFLTVLGKSS 142

RESULT 13
QYH6B4 PRELIMINARY; PRT; 373 AA.
AC QYH6B4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CDNA: FLJ22415 fis, clone HRC08561 (Hypothetical 41.3 kDa protein).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE;
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK026068; BAB15347.1; -.

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DR EMBL; BC009371; AA09371.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00410; IGc2; 2.
DR SMART; SM00410; IG like; 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 373 AA; 41280 MW; FDA215EB3B34335 CRC64;

Query Match 27.9%; Score 378.5; DB 4; Length 373;
Best Local Similarity 34.6%; Pred. No. 1.1e-25;
Matches 91; Conservative 53; Mismatches 104; Indels 15; Gaps 7;

QY 1 MALLCFVLCCGVADLTRSLITTPQMIKAKGETAYLPCRTFLGPDQGLDIEWLIS 60
Db 1 MSLLLLLLL---VSYVVGTLGTHTE---IKRVAEEKVTLPCHHQLGPEKDTLDIEWLLT 54

QY 61 PADNOKVDQVILYSGDKIYDDYODLKGKVHFTSNDLKSGLASINVTNLQSLDICTYQC 120
Db 55 --DNEGQKVITYSSRHVNNLTTEQGRVAFASNFL-AGDASLOIEPLKPSDEGRYTC 111

QY 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIEI GNDFKLCEPKESGLPLLYEWOKL-- 178
Db 112 KVKNSGRYVWSHVILKVLVRPSKPKCELGELTEGSDLTLCQESSSGTEPIVYVQRIRE 171

QY 179 --SNSOKLPTLWLAEMTSP-VISVKNASTEYSGTCTVKNRVGSDQCLRLDVPVPSNR 235
Db 172 KEGEDERLPKSRIDYNHFRVLLQNLTWISYGLYQCTAGNEAGKESCVRV-TVQYVOS 230

QY 236 ACTIAGAVIGVLLALVLIHGLIIF 258
Db 231 IGMVAGAVTGVAGALLIIFLVW 253

RESULT 14
QYH373 PRELIMINARY; PRT; 373 AA.
AC QYH373;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE RIKEN cDNA 9030425E11 gene.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026447; AA026447.1; -.
SQ SEQUENCE 373 AA; 41214 MW; 9C6288484AF95512 CRC64;

Query Match 27.0%; Score 366.5; DB 11; Length 373;
Best Local Similarity 35.3%; Pred. No. 1.3e-24;
Matches 83; Conservative 48; Mismatches 95; Indels 9; Gaps 5;

QY 29 IEKAKGETAYLPCRTFLGPDQGLDIEWLLSPADNOKVDQVILYSGDKIYDDYQDLK 88
Db 22 IKRVAEEKVTLPCHHQLGPEKDTLDIEWLLT--DNEGQKVITYSSRHVNNLTTEQK 79

QY 89 GRVHFTSNDLKSGLASINVTNLQSLDICTYQCKVKAPGVGNKKIQLTVLLKPSGTRCYV 148
Db 80 GRVAFASNFL-AGDASLOIEPLKPSDEGRYTCVKVNSGRYVWSHVILKVLVRPSKPKCEL 138

QY 149 DGSEIEI GNDFKLCEPKESGLPLLYEWOKL---SNSOKLPTLWLAEMTSP-VISVKNAS 203
Db 139 EGEPTEGSDLTLCQESSSGTKPIVYVQRIREKEGEDEHLPPKSRIDYNHFRVLLQNL 198

QY 204 TEYSGTYSCTVKNRVGSDQCLRLDVPVPSNRAGTIAGVIGVLLALVLIHGLIIF 258

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Db 199 MASSGLYQCTAGNEAGKESCVRV-TVQYVQSIGMWAGAVTGIVAGALLIFLLIW 252

RESULT 15

Q920S5 PRELIMINARY; PRT; 373 AA.
AC Q920S5; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Adipocyte-specific protein 5.
GN ASP5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsuruga H.;
RT "Adipocyte-specific protein 5, a novel protein upregulated during
RT adipocyte differentiation.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040490; BAB68503.1;
DR InterPro; IPR003006; I9_MHC.
DR Pfam; PF00047; I9; 2.
SQ SEQUENCE 373 AA; 41186 MW; 5C6280584AF95326 CRC64;

Query Match 26.7%; Score 362.5; DB 11; Length 373;
Best Local Similarity 34.9%; Pred. No. 3.1e-24;
Matches 82; Conservative 48; Mismatches 96; Indels 9; Gaps 5;
QY 29 IEKAKGETAYLPCRFTLGPEDQGLDIEWLLSPADNQKVDVILYSGDKIYDDYQDLK 88
Db 22 IKRVAEKVTLPCHHQLGLPEKOTLDIEWLLT--DNEGKQKVITYSSRHVYNNLTTEEOK 79
QY 89 GRVHFTSNDLKGSDASINVTNLOLSDIGTYQCKVKAPGVGNKKIQLTVLLKPSGTRCYV 148
Db 80 GRVAFASNFL-AGDASIQIEPLKPSDEGRYTCVKQNSGRYVWGVSHVILKALVRPSKPKCEL 138
QY 149 DGSEEEIGNDFKLCEPKEGSLPLLYEWOKL---SNSOKLPTLWLAEMTSP-VISVKNAS 203
Db 139 EGEPTGSDTLQCESASGKPIVYVWQRIREKEGEDEHLPPKSRIDYNNPGRVLLQNL 198
QY 204 TEYSGTYSCTVKNRVGSQCLRLDLVVPPSNRAGTIAGAVIGVLLALVLIIGLIIF 258
Db 199 MASSGLYQCTAGNEAGKESCVRV-TVQYVQSIGMWAGAVTGIVAGALLIFLLIW 252

Search completed: July 9, 2003, 12:45:29
Job time : 34 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 11:13:22 ; Search time 1878 seconds
(without alignments)

404.639 Million cell updates/sec

Title: US-09-899-634c-2

Perfect score: 1359
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Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-FEAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*

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41: em_hcg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1341	98.7	959	4	AF109646 Sus scrofa
2	1270	93.5	1184	4	AY033651 Bos taurus
3	1254	92.3	959	4	AF109645 Canis fam
4	1238	91.1	1033	9	AF124598 Homo sapi
5	1238	91.1	2354	9	HSU90716 Human cell
6	1238	91.1	2434	6	ARI57886 Human cell
7	1238	91.1	2434	9	HS46KDA
8	1238	91.1	2537	9	BC010536 Homo sapi
9	1238	91.1	2537	9	BC003684 Homo sapi
10	1238	91.1	3060	6	AX055476 Sequence
11	1238	91.1	3060	6	AX089948 Sequence
12	1238	91.1	3060	6	AX358962 Sequence
13	1238	91.1	3060	6	AX362455 Sequence
14	1238	91.1	3060	6	AX403617 Sequence
15	1238	91.1	3060	6	AX454694 Sequence
16	1238	91.1	3060	6	AX491172 Sequence
17	1238	90.7	1333	10	AX098210 Sequence
18	1233	90.7	1076	10	AF109643 Rattus no
19	1233	90.1	1095	6	AF109644 Rattus no
20	1224	90.1	1584	6	ARI44703 Sequence
21	1224	90.1	1584	6	ARI44702 Sequence
22	1216	89.5	1098	10	MMU90715 Mus musculus
23	1216	89.5	1206	10	MMU90715 Mus musculus
24	1216	89.5	1515	6	ARI44704 Sequence
25	1216	89.5	1669	10	NMCCAROM Mus musculus
26	1216	89.5	1669	10	NMCCAROM Mus musculus
27	1145	84.3	170558	2	AC012414 Homo sapi
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29	1133	83.4	108122	2	AC116905 Homo sapi
30	1131	83.2	167605	2	AC068446 Homo sapi
31	1131	83.2	174104	2	AC060814 Homo sapi
32	1103.5	81.2	152318	2	AL162851 Homo sapi
33	1103.5	81.2	166239	9	HS214614 Homo sapi
34	1103.5	81.2	340000	9	HS214614 Homo sapi
35	921	67.8	759	9	AY072912 Homo sapi
36	875	64.4	64976	2	AC026256 Homo sapi
37	676	49.7	603	9	AY072911 Homo sapi
38	659.5	48.5	1883	5	AF268197 Danio rer
39	641	47.2	1312	10	BC004680 Homo sapi
40	407	29.9	1296	9	AB079879 Homo sapi
41	402.5	29.6	1805	9	BC034411 Homo sapi
42	400.5	29.5	1287	10	AB079880 Homo sapi
43	378.5	27.9	2307	9	BC009371 Homo sapi
44	378.5	27.9	2458	6	AX358876 Sequence
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RESULT 1

ALIGNMENTS

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LOCUS	AFI09646				
DEFINITION	Sus scrofa coxsackie-adenovirus-receptor homolog (CAR) mRNA,				
ACCESSION	AFI09646				
VERSION	AFI09646.1	GI:6013138			
KEYWORDS	.				
SOURCE	Sus scrofa.				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
REFERENCE	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
AUTHORS	Fechner,H., Haack,A., Wang,H., Wang,X., Eicema,K., Pausinger,M., Schoemaker,R., Veghel,R., Houtsmuller,A., Schultzeiss,H.P., Lamers,J., and Poller,W. Expression of coxsackie adenovirus receptor and alpha-v integrin does not correlate with adenovector targeting in vivo indicating anatomical vector barriers				
TITLE	Gene Ther. 6 (9), 1520-1535 (1999)				
JOURNAL	99422053				
MEDLINE	10490761				
PUBMED	2 (bases 1 to 959)				
REFERENCE	Fechner,H., Haack,A., Wang,H., Wang,X., Wiese,A., Lamers,J.M.J. and Poller,W. Direct Submision Submitted (25-NOV-1998) Department of Cardiology and Pneumology, Benjamin Franklin University Hospital, Hindenburgdamm 30, Berlin 12200, Germany				
AUTHORS	Location/Qualifiers				
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ORIGIN					
Alignment Scores:					
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Percent Similarity:	99.62%	Conservative:	1		
Best Local Similarity:	99.23%	Mismatch:	1		
Query Match:	98.68%	Indels:	0		
DB:	4	Gaps:	0		
US-09-899-634C-2 (1-261) x AFI09646 (1-959)					
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Db	1 ATGGCGTTTCGTCCGCTCGCTCGCTCGTGTGAATCGCGGATCTCACCAAAATTGG 60				
OY	21 Ser1etrrrrPrroGluglMetlllegluysalalygylgnluthAlAtyrleuPro 40				
Db	61 AGTACTACTACTCCGGAACAGATGATTGAAAAGGCCCAAAGGGGAAACCTCATTTGGCG 120				
OY	41 CysArqPhetnLeuGjYProgluAspgInglYProLeuAspi1leglTrpLeuLeusenr 60				
Db	121 TGCAGATTTAACCTCGGTCCAGAAACCAGGGGCGCGTGCAGATCGATGCTGCTGTC 180				
OY	61 ProAlaAspAmglnllyValaspGlnVallelleleuTyrseryGlyAspLyslleTyrr 80				

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Alignment Scores:				
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DB:	4	Gaps:	0	
US-09-899-634C-2 (1-261) x AY033651 (1-1184)				
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Db	1	ATGGAGCTTTCGCTGCGGCTTCCTTCCTTCGCGAGTGGGGAATTTCACAGAGGCTTG	60	
QY	21	SerIleThrTrpProGluGlnMetIleGluIysAlaIysGlyGluThAlaTyIleuPro	40	
Db	61	AGTATCATTACTCTCGAAGCAGTGAATTAAAGGCAAGGGGAAACGCTTATTGGCA	120	
QY	41	CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluTrpLeuLeuSer	60	
Db	121	TGCAAAATTACCCTGGGTCCGGAACACAGGGGCTTCGACATGATGCTGCTGCA	180	
QY	61	ProAlaAspAsnGlnIysValAspGlnValIleIleuTySerGlyAspLysIleTy	80	
Db	181	CCAGCTGATTAATCAGMAGGTGATCAAGTGAATTATTATTAATTCGAGACAAATTTAT	240	
QY	81	AspAspTyTrpGlnAspLeuIysGlyArgValHisPheThrSerAsnAspLeuIysSer	100	
Db	241	GATGACTCTATCAAGACTCTGAAGAGCAGTACATTTTCAAGTATGATCTCAAACT	300	
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Db	301	GGTGATGCTTCAATTAATGTGCAAAATTTACAGCTGCAGATATTTGCACATATCAGTGC	360	
QY	121	LysValIleIysIleAspProGlyValGlyAsnLysIleGlnLeuThValleuLeuLys	140	
Db	361	AAAGGAAAAAAGCCTCGGTGGTGAATAAGAAATTCAGCTCAGCTTCCTGTTAAG	420	
QY	141	ProSerGlyThrArgCysTyValAspGlySerGluGluIleGlyAsnAspPheIysLeu	160	
Db	421	CCTTCAGGTATACATGTATTATGTTATGATCAGCAAGAAATTGGAAAGACCTTTAACTC	480	
QY	161	LysCysGluProLysGluGlySerLeuProLeuLeuTyrgIuTrpGlnLysLeuSerAsn	180	
Db	481	AAATGTGAACCAAAAGAGGTTCACCTCCACATGACATATGATGACAGATATCCGAC	540	
QY	181	SerGlnLysLeuProThrLeuTrpLeuAlaGluMetThrSerProValIleSerValLys	200	
Db	541	TCACAGAAACGTGCCACCTCTGTGTATTCACAGAAAGACATCACCTGTATATCTGTGAAA	600	
QY	201	AsnAlaSerThrGluTySerGlyThrTySerCysThrValIysAsnArgValGlySer	220	
Db	601	AATGCGATGCCGATTACTCCGGGACATACACTTACGGTCAGAAACAGAGTGGGCTCT	660	
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Db	661	GATCAGTCCCTGCTCGCTGGATGTGCTTCCTCTCAACACAGAGCGGACCAATTGCA	720	
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Db	721	GGAGCTGTATAGGAACCTTGCTTCGCTTGCTTATTCCTTATATGCTCTTTTGCGGT	780	

LOCUS	AF109645	959 bp	mRNA	linear	MAM 06-OCT-1999
DEFINITION	Canis familiaris coxsackie-adenovirus-receptor homolog mRNA.				
ACCESSION	AF109645				
VERSION	AF109645.1	GI:6013136			
KEYWORDS					
SOURCE	Canis familiaris.				
ORGANISM	Canis familiaris				
REFERENCE	Mammalia; Eutheria; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
AUTHORS	1 (bases 1 to 959) Fechner,H., Haack,A., Wang,H., Wang,X., Wiese,A., Pauschinger,M., Schoenaker,R., Veghel,R., Houtsmuller,A., Schulteis,H.P., Lamers,J. and Poller,W.				
TITLE	Expression of coxsackie adenovirus receptor and alphav-integrin does not correlate with adenovector targeting in vivo indicating anatomical vector barriers				
JOURNAL	Gene Ther. 6 (9), 1520-1535 (1999)				
MEDLINE	99422053				
PUBMED	10490761				
REFERENCE	2 (bases 1 to 959) Fechner,H., Haack,A., Wang,H., Wang,X., Wiese,A., Lamers,J.M.J. and Poller,W.				
AUTHORS	Direct Submission				
TITLE	Submitted (24-NOV-1998) Department of Cardiology and Pneumology, Benjamin Franklin University Hospital, Hindenburgdamm 30, Berlin 12200, Germany				
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VERSION   AF124598.1 GI:4884701
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AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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          Fechner,H., Haack,A., Wang,H., Wang,X., Bizema,K., Pauschinger,M.,
          Schomaker,R., Vechtel,R., Houtemuller,A., Schultheis,H.P.,
          Lamers,J. and Poller,W.
          Expression of coxsackie adenovirus receptor and alpha-v-integrin
          does not correlate with adenovector targeting in vivo indicating
          anatomical vector barriers
          Gene Ther. 6 (9), 1520-1535 (1999)
JOURNAL  99422053
MEDLINE  10490761
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REFERENCE 2 (bases 1 to 1033)
AUTHORS  Fechner,H., Haack,A., Wang,H., Wang,X., Wiese,A., Lamers,J.M.J. and
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          Direct Submission
          Submitted (29-JAN-1999) Department of Cardiology and Pneumology,
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JOURNAL	Tomko, R.P., Xu, R. and Philipson, L.				
MEDLINE	HCR and MCR: the human and mouse cellular receptors for subgroup				
PUBMED	C adenoviruses and group B coxsackieviruses				
REFERENCE	Proc. Natl. Acad. Sci. U.S.A. 94 (7), 3352-3356 (1997)				
AUTHORS	97250541				
TITLE	2 (bases 1 to 2354)				
JOURNAL	Tomko, R.P., Xu, R. and Philipson, L.				
MEDLINE	Direct Submission				
PUBMED	Submitted (24-FEB-1997) Structural Biology, Skirball Institute for				
REFERENCE	Biomolecular Medicine, New York University Medical Center, 550				
AUTHORS	First Avenue, New York, NY 10016, USA				
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 AUTHORS Strausberg, R.
 TITLE Direct Submission
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 COMMENT Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: http://www.shgc.stanford.edu
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.
 Clone distribution: MGC clone distribution information can be found
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      Db      497  CTTTCAGGTGCGAGATGTTTACGTTGATGATCTGAGAAATTTGAGAGTGCATTTAAGATA 556
      QY      161  LysCySGluProLysGlnGlySerLeuProLeuLeuTYrGluTYrGlnLysLeuSerAsn 180
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      QY      181  SerGlnLysLeuProThrLeuTYrPLeuAlGluMetHisSerProVal1IeSerValLys 200
      Db      617  TCACAGAAATGCCCACTTCATGTGTAGCAGAAATGACCTTCATCTGTATATCTGTAAAA 676
      QY      201  AsnAlaSerThrGluTYrSerG1YThrTYrSerCySthrValLysAsnArgValG1YsSer 220
      Db      677  AATGCCCTCTTCTGAGTACTGTGGACATACAGCTGACAGTCAAGTCAAGAGAGGGGCTCT 736
      QY      221  AspGlnCySLeuLeuArgLeuAspValValProProSerAsnArgAlaG1YThr1IeAla 240
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      QY      261  Arg 261
      Db      857  CGT 859

RESULT 12
LOCUS      AX358962              3060 bp      DNA      linear      PAT 13-FEB-2002
DEFINITION Sequence 215 from Patent WO0193983.
ACCESSION  AX358962
VERSION     AX358962.1  GI:18675382
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
  1  Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
      Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
      Watanabe,C.K. and Wood,W.I.
      Secreted and transmembrane polypeptides and nucleic acids encoding
      the same
      Patent: WO 0193983-A 215 13-DEC-2001;
      Genentech Inc. (US)
FEATURES
  source     1..3060
             Location/Qualifiers
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
BASE COUNT  1094 a      559 c      569 g      837 t      1 others
ORIGIN
Alignment Scores:
Pred. No.: 2,61e-112      length: 3060
Score: 1238.00      Matches: 233
Percent Similarity: 94.25%      Conservative: 13

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Best Local Similarity: 89.27%      Mismatches: 15
Query Match: 91.10%      Indels: 0
DB: 6      Gaps: 0
US-09-899-634c-2 (1-261) x AX358962 (1-3060)

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      QY      21  Ser1IeThrThrProGlnGlnMet1IegLYLysAlaLysGlyGluThrAlaTYrLeuPro 40
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      QY      41  CyArgPheThrLeuG1YProGlnAspGlnG1YProLeuAsp1IegLYThrPLeuLeuSer 60
      Db      197  TCGAAATTAACCTTATGCTCCGAGACCGAGGACCGCTGACATCAGTGGCTGATATCA 256
      QY      61  ProAlaAspAsnGlnLysValAspGlnVal1IeIleLeuTYrSerG1YAspLys1IeTYr 80
      Db      257  CCGAGCTGATATACAGAGGTGATCAAGTATTATTATTTATCTGAGACAAATTTAT 316
      QY      81  ASPASPTTYTTCGlnAspleuYsgLYArGVaIHIsphethSerAsnAspleuYsSer 100
      Db      317  GATGACTACTATCCAGATCTTGAAAGGCCGAGTACATTTTACAGATATGATCTCAAAATCT 376
      QY      101  GLYAspAlaSer1IeAsnValThrAsnLeuGlnLeuSerAsp1IegLYThrTYGlnCys 120
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      QY      141  ProSerG1YThrArGcYsTYrValAspG1YSerGlnGlu1IegLYAsnAspPheLYsLeu 160
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      QY      161  LysCySGluProLysGlnGlySerLeuProLeuLeuTYrGluTYrGlnLysLeuSerAsn 180
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      QY      181  SerGlnLysLeuProThrLeuTYrPLeuAlGluMetHisSerProVal1IeSerValLys 200
      Db      617  TCACAGAAATGCCCACTTCATGTGTAGCAGAAATGACCTTCATCTGTATATCTGTAAAA 676
      QY      201  AsnAlaSerThrGluTYrSerG1YThrTYrSerCySthrValLysAsnArgValG1YsSer 220
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      QY      221  AspGlnCySLeuLeuArgLeuAspValValProProSerAsnArgAlaG1YThr1IeAla 240
      Db      737  GATCAGAGCTGTGTGGCTTAAAGCTTGCCCTCCCTCAATTAAGCTGACATTAATGCA 796
      QY      241  GlyAlaVal1IegLYValLeuLeuAlaLeuValLeu1IegLYLeu1IeIlePheCYs 260
      Db      797  GAGGACATTAATGAACTTTGCTGTCTAGCGCTCATTTGCTTATCATCTTTTGTCTGT 856
      QY      261  Arg 261
      Db      857  CGT 859

RESULT 13
LOCUS      AX362455              3060 bp      DNA      linear      PAT 15-FEB-2002
DEFINITION Sequence 215 from Patent WO0208288.
ACCESSION  AX362455
VERSION     AX362455.1  GI:18694685
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE	Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
AUTHORS	Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
TITLE	Watanabe,C.K. and Wood,W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL	Patent: WO 0208288-A 215 31-JAN-2002;
FEATURES	Genentech, Inc. (US)
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Alignment Scores:	
Pred. No.:	2,61e-112 Length: 3060
Score:	1238.00 Matches: 233
Percent Similarity:	94.25% Conservative: 13
Best Local Similarity:	89.27% Mismatches: 15
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Db	77 ATGGCGCTCTCGTGCCTTCGGCTCCGTGGAGAGTAGTGATTCCGCCAGAAGTTTG 136
OY	21 SerIlethrThProGlunMetIleGluValAlaLysGlyLuhraIatYleuPro 40
Db	137 AGTATCACACACCCTCGMAAGATGATTGA AAAAGCCAAAGGGGAAA CTGCTTATCGCCA 196
OY	41 CysAtgPheThrLeuGlyProGluAaspGngIProLeuAspiIlegIutPleuLeuSer 60
Db	197 TGCAAAITTTACGCTTAGTCTCCGAGACCGAGACCCCTGGACATCGAGTGGCTGATATCA 256
OY	61 ProAlAasPasGlnLysValAspGlnValIleIleLeuLysSerGlyAspLysIleYr 80
Db	257 CCAGCTGATTAATCAGAGGTGGATCAAGGATTTATTTATTTATTCGTGAGACAATAATTAT 316
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Db	317 GATGACTACTATCCAGATCTGAAAGGCCAGATCATTTTAACGATATGATCTCAATCT 376
OY	101 GlyAspAlaSerIleasnValThrAnLeuGlnLeuSerAspiIlegIyThrTYrGlnCyS 120
Db	377 GGATGATGATCAATAAATTAACGAATTTAACACTGCAATTTGGCATATTCAGTGC 436
OY	121 LysValILysValAlAProGlyValIGlYasnLysLysIIlgIleuThrValIleuLeuLys 140
Db	437 AAAGTGA AAAAGCTCTGATGTGGCAAAATACAAATTCATCTGGTAGTTCTTGTAAG 496
OY	141 ProSerGlyThrArgCysTYrValAspGlySerGluGlnIlegLYasnAspPheLysLeu 160
Db	497 CCTTCAGGTCGAGATGTTACGTTGATGTGATCGAAGAAATTCGAGTACTTAAGATA 556
OY	161 LysCySGluProLysGluGlySerLeuProLeuLeuTYrGluTrpGlnLysLeuSerAsn 180
Db	557 AAATGTGAACCAAAGAAAGTTCACCTTCATTACACTAGACGAGGCAAAAATGTCTGAC 616
OY	181 SerGlnLysLeuProThrLeuTrpLeuAlaGluMetThrSerProValIIeserValIys 200
Db	617 TCACGAAAAATGCCACTTCATGATGAGCAAGAAATATCACTCTGTATATCTGTAAA 676
OY	201 AsnaIaseThrGluTYrSerGlyThrTYrSerCySThrValIysAsnArgValIGlySer 220
Db	677 AATGCTCTTCGAGACTCTGGGACATACAGCTGTACACTCGAACAACAGAGTGGCTCT 736
OY	221 AspGlnCyLeuLeuArgLeuAspValValProProSerAsnArgIaagIyThrIleIla 240
Db	737 GATCAGTGCCTGTGGGTCTAAACGTTGTCCTCTTCAAAATAAGCTGCAATATTGCA 796

OY		241	G V A L A V A I E G I V A L L E U L E A L D E V A L L E U L E G I V A L L E I P H C Y S C S	266
Dd		797	GGAGCCATTAAGGAACCTTGCTTGTCTGTACCGCTCAATTGTCITTAICATCTTTGCTGT	856
OY		261	Arg	261
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		SOURCE	human.	
		ORGANISM	Homo sapiens	
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			Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
		REFERENCE		
		AUTHORS	1 Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,	
			Ferrara,N., Gerber,H., Gjeritsen,M., Goddard,A., Godowski,P.,	
			Grimaldi,C.U., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,	
			Pooni,N.F., Roy,M., Stewart,T.A., Tamas,D., Watanabe,C.K.,	
			Williams,P., Wood,W.I. and Zhang,Z.	
		TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding	
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		JOURNAL	Patent: WO 0073454-A 504 07-DEC-2000;	
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OY		21	SeRIethrThrProGLUGInMetIElEGULysAlALysGLIGurThAlATyrLeuPro	40
Dd		137	AGTATCACTACTCTCTGAAGAAGATGATTGA AAAAGCCA AAAGGGAAACTGCTTACTGCCA	196
OY		41	CysArGPheThrLeUGLyProGLUApgINGLyProLeuAspIIeGUtTrpLeuLeuSer	60
Dd		197	TGC A A A T T T A C G C T T A C C C G A A G A C C A G C C G T G C A C A T C G A T A T A C A	256
OY		61	ProAlAAspANGInLysValASpGINValIIelLeULeuTYrSERGIYAapLVAlETyr	80
Dd		257	CCACTGATTAATCA GAAGGTGATCAACTGATTTATTTTATTTCTTGAGACAAAATTTAT	316
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Dd		317	GATGACTTAATAATCCAGATTCGA AAGCGCATCATTTTACGATTAATGATCTCAAATCT	376
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Dd		377	GGTATGATCAATCAATTAATGTAA CGAATTTTCAACGTCTCAGATATTGGCACATATCAAGTGC	436
OY		121	LysValLysLysAlAProGLIVAlGLYASNlysLysLIeGLIneuThrValLeULeULys	140
Dd		437	AAAGTGA AAAAGTCTCTGGGTGGTTCGAATTAAGAAAGATTATCTGGTAGTCTTGTTAAG	496

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES						
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3	1238	91.1	2434	24	ABL60622	Human coxsackie-a3
4	1238	91.1	2960	24	ABL88211	Human PRO5723 CDN
5	1238	91.1	3059	24	ABL95700	Human angiogenesis
6	1238	91.1	3060	22	AAAD03924	Human PRO5723 CDN
7	1238	91.1	3060	22	AAAF44263	Human PRO5723 nuc
8	1238	91.1	3060	22	AAAC91448	Human PRO5723 CDN
9	1238	91.1	3060	24	ABK33643	cDNA encoding hum
10	1238	91.1	3276	22	AAFP88715	Human late stage
11	1238	91.1	3963	23	AAV25520	Human prostate ex
12	1224	90.1	1584	19	AAV28845	Human coxsackiev
13	1216	89.5	1128	19	AAV28846	Mouse coxsackiev
14	1216	89.5	1301	19	AAV50430	Mouse coxsackiev
15	1142	84.0	795	20	AAV72025	Adenovirus PAC7SG
16	1142	84.0	834	20	AAV72026	Adenovirus SCAR
17	1142	84.0	1194	20	AAV72027	Adenovirus PACSG2
18	800	58.9	578	22	AAH76081	Rat coxsackie-aden
19	407	29.9	1758	22	ABA06581	Human CDNA SEQ ID
20	407	29.9	1853	22	AA528826	Human immunoglob
21	395	29.1	762	24	ABO54554	Human ovarian ant
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23	378.5	27.9	1122	22	AAAC84384	Human A236 polyep
24	378.5	27.9	1948	22	AAAC84383	Human A236 polyep
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32	378.5	27.9	2458	24	ABL95592	Human angiogenesi
33	378.5	27.9	2458	24	ABL88103	Human PRO363 CDNA
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36	366.5	27.0	1122	22	AAAC84392	Mouse A236 polyep
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38	366.5	27.0	1949	22	AAAC84416	Mouse A236 varian
39	363.5	26.7	1949	22	AAAC84418	Mouse A236 varian
40	362.5	26.7	1937	22	AAH76376	Murine adipocytes
41	357	26.3	811	22	ABA06752	Human cDNA SEQ ID
42	357	26.3	811	22	AA528873	Human immunoglob
43	351.5	25.9	2565	18	AAAT62369	Human A33 antigen
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RESULT 1

AAV50429

ID AAV50429 standard; CDNA; 2354 BP.

AAV50429;

07-DEC-1998 (first entry)

Human coxsackievirus and Ad2 and Ad5 receptor (HCAR) CDNA.

HCAR; coxsackievirus receptor; CVB; adenovirus; Ad2 receptor;

Ad5 receptor; human; infection; vaccine; gene therapy; ds.

Homo sapiens.

key Location/Qualifiers

CD5 1..1098

PT /*tag= a

ALIGNMENTS

OS Homo sapiens.
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 PN W0200208288-A2.
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 PD 31-JAN-2002.
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 PF 29-JUN-2001; 2001WO-US21066.
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 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
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 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220646P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001WO-US17092.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 DR WPI; 2002-172001/22.
 DR P-PSDB; AAU83699.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT tumour or liver tumour -
 XX
 PS Claim 2; Figure 215; 359pp; English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human
 CC PRO protein coding sequences of the invention.
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 SO Sequence 3060 BP; 1094 A; 559 C; 569 G; 837 T; 1 other;
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 Pred. No.: 8,19e-123 Length: 3060
 Score: 1238.00 Matches: 233
 Percent Similarity: 94.25% Conservative: 13
 Best Local Similarity: 89.27% Mismatches: 15
 Query Match: 91.10% Indels: 0
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QY 1 MetAlaLeuLeuLeuCySpHeValLeuLeuCyGlyValAlaAspLeuThrArgSerLeu 20
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 QY 41 CysArgPheThrIleGluLysProGluAspGlnGlyProLeuAspIleGluTyrLeuLeuSer 60
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 QY 61 ProAlaAspAsnGlnLysValAspGlnValIleIleLeuTyrSerGlyAspLysIleTyr 80
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 DB 737 GATCAGTGGCTGTGGCTCTAAACGTTGCTCCCTTCAAAATAAAGCTGCACTAATTGCA 796
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 AC AAF98715;
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 DT 02-JUL-2001 (first entry)
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 KW Human; ovarian cancer; identification; detection; characterisation;
 XX tumour; kinase; marker; cytostatic; antisense gene therapy; de.
 OS Homo sapiens.
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US-09-899-634C-2 (1-261) x AAV28845 (1-1584)

Qy		1	MetAlaleuleuleucysPheValleuleucYsgilyValAlaAspleuthArgSerLeu	20
Db		60	ATGGCGCTCCGTGCTGCTTCGTGCCTCGTCCGAGTAGTGGAATTGCCAAGAAGTTTG	119
Qy		21	SerIleThrProGluInMetIleGlyLysAlaLysGlyGluThrAlaTYrLeuPro	40
Db		120	AGATCACTACTCTCTTAAGAAGATGTGAAAAAGCCAAGGGGAAACCTCATCTCCG	179
Qy		41	CysArgPheThrLeuGlyProGluAspGlnGlyProLauAspIleGluTrpLeuLeuSer	60
Db		180	TGCMAATTTTACGGCTAGGCTCCCGAAGACCAGGACCGCTGACATCGAGTGCATATCA	239
Qy		61	ProAlaAspAsnGlnLysValAspGlnValIleIleLeuTYrSerGlyAspLysIleTYr	80
Db		240	CCAGCTGATATATCAGAAGGTGGATCAAGATATTATTATTTATTCGGAGACAATAATTAT	299
Qy		81	AspAspTYrTYrGlnAspleuleuysglyArgValHisPheThrSerAsnAspLeuLysSer	100
Db		300	GATGACTACTATCCAAATCTGAAGATCGAAGGCCAGATACATTTTACAGAAATGATCCAAATCT	359
Qy		101	GlyAspAlaSerIleLeuValThrAsnLeuGlnLeuSerAspIleGlyTYrThrGlnCys	120
Db		360	GGGATGATCACTAAATTAATGATTAACGAATTTTACAACGTCAAGATTTGGCACATATCAATG	419
Qy		121	LysValLysLysAlaProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLys	140
Db		420	AAAGTGAATAAACCTCTGCTGTGCAATTAAGAAATCCATCTGCTGTTGTTGTTAG	479
Qy		141	ProSerGlyThrArgCysTYrValAspGlySerGluGluIleGlyAsnAspPheLysLeu	160
Db		480	CTTTCAAGTGCAGATGTTTACGTGATGTGATCGAAGAAATGGAAAGTCACTTTAAGATA	539
Qy		161	LysCysGluProLysGluGlySerLeuProLeuLeuTYrGluTrpGlnLysLeuSerAsn	180
Db		540	AAATGTGAACCAAAGAAGGTTCACTTCATTACAGTATGAGTGGCAAAAATTCCTGAC	599
Qy		181	SerGlnLysLeuProThrLeuThrLeuPleuAlaGluMetThrSerProValIleSerValLys	200
Db		600	TCAACAGAAATGCCCCACTTCATCGTTAGAGAAATGACTCATCTGTTATATCTGTAAAA	659
Qy		201	AsnAlaSerThrGlnLysSerGlyTYrTYrYSerCysThrValLysAsnArgValAlaGlySer	220
Db		660	AATGCTCTTCTGAGTACTCTGGGACATACACAGCTGACGTACGAACAAAGAGTGGCTCT	719
Qy		221	AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIleAla	240
Db		720	GATCAGTGCTGTTGGGTCTAAACGTTGCTCTCTCTCAAAATAAAGCTGAGCTAATTGCA	779
Qy		241	GlyAlaValIleGlyValLeuLeuAlaLeuValLeuIleGlyLeuIleIlePheCysCys	260
Db		780	GGAGCCATTTATAGAACTTTGCTGCTCAGCGCTCATGTCCTTATCATCTTTTGCTGT	839
Qy		261	Arg 261	
Db		840	CGT 842	

RESULT 13
ID AAV28846 standard; DNA: 1128 BP.
NC AAV28846;
XX

DT	03-AUG-1998	(first entry)
XX		
DE	Mouse.	coxsackievirus and adenovirus receptor encoding DNA.
XX		
KM	Mouse; coxsackievirus; adenovirus; receptor; CAR; cardiac infection;	
KM	myocarditis; pericarditis; dilated cardiomyopathy; meningoencephalitis	
KM	pancreatic infection; acute pancreatitis; gastrointestinal tract;	
KM	diabetes mellitus; ss.	
XX		
OS	Mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..1128
FT		/tag= "a
FT		/product= "coxsackievirus and adenovirus receptor"
FT		/transl_except= (pos:1096..1998,aa:xa)
FT		/note= "Xaa= a stop codon, the sequence is shown as
FT		continuing but gets unclear"

CC The present sequence encodes mouse coxsackievirus and adenovirus
 CC receptor (CAR). The present invention also describes: (1) a method for
 CC modulating CAR expression comprising contacting the cell with an agent
 CC which modulates CAR protein activity or CAR nucleic acid expression,
 CC such that a cell associated activity is altered relative to a cell
 CC associated activity of the cell in the absence of the agent; and (2) a
 CC method for detecting the presence of CAR in a biological sample
 CC comprising contacting a biological sample with an agent capable of
 CC detecting CAR protein or mRNA such that the presence of CAR is detected.
 CC Modulation of CAR is useful for treatment of cardiac infection, e.g.
 CC myocarditis, pericarditis or dilated cardiomyopathy, or infection of the
 CC central nervous system, e.g. a non-specific febrile illness or
 CC meningoencephalitis, or pancreatic infection, e.g. acute pancreatitis,
 CC or infection of the respiratory or gastrointestinal tract or childhood
 CC onset diabetes mellitus. Probes derived from CAR nucleic acids are
 CC useful for hybridization assays, and antibodies raised against CAR
 CC protein are useful for blocking CAR expression. Cell-free assays which
 CC include combining CAR protein and a candidate/test compound are useful
 CC in screening for drugs which interact with CAR protein.

XX
 SQ Sequence 1128 BP; 297 A; 286 C; 288 G; 257 T; 0 other;

Alignment Scores:

Pred. No.:	4,76e-121	Length:	1128
Score:	1216.00	Matches:	229
Percent Similarity:	93.85%	Conservative:	15
Best Local Similarity:	98.08%	Mismatches:	16
Query Match:	89.48%	Indels:	0
DB:	19	Gaps:	0

US-09-899-634C-2 (1-261) x AAIV28846 (1-1128)

QY 1 MetAlaLeuLeuLeuCySpheValLeuLeuCyGlyValAlaAspIeuThraTrSerIeu 20

```

Db      1 ATGGCCGGCCTACTGCTGCTTCTGCTTGTGGCGGATCGCGGATTTTCACAGTGGTTTG 60
Qy      21 Ser1eThrThProgluInMet1leglulysAla1ysgluThralaTyLeuPro 40
Db      61 AGCATCACTACACCCGACAGAGAGATGAAAAACCAAGGGAACTGGCTATCTTACCA 120
Qy      41 CysArgPheThrLeuGlyProgluAspGlnGlyProLeuAsp1leglulThLeuSer 60
Db      121 TGCAGATTACTCTCAGCTCCCGAAGACAGGAGACCACTGACATTTGAATGCTGATATCC 180
Qy      61 ProAlaAspAsnGlnysValaAspGlnVal1lelleuTySerGlyAsp1ys1leTy 80
Db      181 CCTCTGATTAACAGATAGTGATCAAGTATATTTGATTTCTGGAGCAAAATTTAT 240
Qy      81 AspAspTyTyTyGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
Db      241 GATTACTACTATCCGATCTGAAAGACGGGTACATTTTCAGATACGATGTCAGTCT 300
Qy      101 GlyAspAlaSer1leAsnVal1ThrAsnLeuGlnLeuSerAsp1leglulThTyGlnCys 120
Db      301 GGGAGCGCATCTATAATGATGACCAACCTGACGCTGCGACATTGGCACTTACCAAGTGC 360
Qy      121 LysVal1ylsValaProgl1yVal1GlyAsnLys1leGlnLeuThrVal1leuLys 140
Db      361 AAAGTGAAAGAACCCCTGGGGGTGGCAAAATAGAAATTCCTGCTGACCGCTTGTTAAG 420
Qy      141 ProSerGlyThrArgCysTyTyValaAspGlySerGlnGln1leglulAsnAspPheLysLeu 160
Db      421 CCTTCAGGTACAGATGCTTCGTGATGATCGGAGAGATTGGAAATGACTTCAACTA 480
Qy      161 LysCysGlnProLysGlnGlySerLeuProLeuLeuTyGlnTyGlnLysLeuSerAsn 180
Db      481 AAATGTGAACCCAAAGGAAGGCTCCCTCCACTACAGTTGAATGGCAAGAACTGTCGAC 540
Qy      181 SerGlnLysLeuProThrLeuThrLeuAlaGlnMetThrSerProVal1leSerValLys 200
Db      541 TCCCAAGCATGCTTACGCGCATGCTGGCAGAAATGACGTACCAAGTTATATCTGTGAAG 600
Qy      201 AsnAlaSerThrGlnTyTySerGlyThTyTySerCysThralysAsnArgVal1GlySer 220
Db      601 AAGCCCGATTCTGATGTTTCTGGACATACAGCTGCGACGGTTCAAAACAGAGTGGGCTCT 660
Qy      221 AspGlnCysLeuLeuArgLeuAspVal1ValProProSerAsnArgAlaGlyThr1leAla 240
Db      661 GACCAAGTGTATGCTGGCAGCTAGAGCTGTCCCAACCTCCCAACGAGCGGAGAGATGCG 720
Qy      241 GlyAlaVal1leGlyVal1leuLeuAlaLeuVal1leu1leGlyLeu1lellePheCys 260
Db      721 GGGCGCTGTATAGGAGCGCTGCTGGCCCTGTGCTCATCGGGGCGCATCTTCTGCTGT 780

```

RESULT 14

AAVS0430
ID AAVS0430 standard; cDNA, 1301 BP.

AAVS0430;
07-DEC-1998 (first entry)

Mouse coxsackievirus and Ad2 and Ad5 receptor (MCAR) cDNA.

MCAR; coxsackievirus receptor; CVB; adenovirus; Ad2 receptor;
KM Ad5 receptor; mouse; infection; vaccine; gene therapy; ds.

OS Mus sp.

Key Location/Qualifiers

FT CDS 157..1215

/*tag= a

PN MO9833819-A1.

PD 06-AUG-1998.

XX

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PF      30-JAN-1998; 98MO-US01724.
XX
PR      30-JAN-1997; 97US-0036986.
XX
PA      (UYNV ) UNIV NEW YORK STATE.
XX
PI      Philipson L, Tomko RP;
XX
DR      WPI; 1998-437397/37.
XX
P-PSDB; AAM69698.
PT      DNA encoding human receptor for adenovirus C and coxsackievirus B -
PT      for preventing and treating viral infection and rendering cells
PT      susceptible to transformation by adenoviral vectors in gene therapy
XX
PS      Claim 2; Page 68-70; 88pp; English.
XX
CC      This cDNA molecule codes for mouse MCAR protein (see AAM69698) that
CC      serves as a cellular receptor for adenoviruses of the serotypes 2
CC      and 5 (subgroup C) and for the group B coxsackieviruses (CVB). It
CC      was obtained by screening a lambda phage expression cDNA library
CC      with antiserum containing antibodies specific for mouse CVB
CC      binding protein p46, and was used to identify human HCAR cDNA
CC      (see AAVS0429). The invention also provides host cells transformed
CC      with DNA molecules encoding HCAR or MCAR and methods of producing
CC      the recombinant proteins or their derivatives. These proteins,
CC      CC their extracellular domains, as well as oligopeptides (see
CC      AAM69699-708) which bind virus, are also provided. Isolated HCAR or
CC      MCAR proteins or their fragments or variants are used to prevent
CC      or treat virus infections. Expressing the DNA in cells which lack
CC      these viral receptors renders the cells susceptible to
CC      transformation by adenoviral vectors carrying genes for gene
CC      therapy.
XX
SQ      Sequence 1301 BP; 355 A; 327 C; 322 G; 297 T; 0 other;

```

Alignment Scores:

Pred. No.: 5.8e-121 Length: 1301
Score: 1216.00 Matches: 229
Percent Similarity: 93.85% Conservative: 15
Best Local Similarity: 88.08% Mismatches: 16
Query Match: 89.48% Indels: 0
DB: 19 Gaps: 0

US-09-899-634c-2 (1-261) x AAVS0430 (1-1301)

```

Qy      1 MetAlaLeuLeuLeuLeuCysPheVal1leuLeuCysGlyVal1AlaAspLeuThrArgSerLeu 20
Db      157 ATGGCCGGCCTACTGCTGCTTCTGCTTGTGGCGGATCGCGGATTTTCACAGTGGTTTG 216
Qy      21 Ser1eThrThProgluInMet1leglulysAla1ysgluThralaTyLeuPro 40
Db      217 AGCATCACTACACCCGACAGAGAGATGAAAAACCAAGGGAACTGGCTATCTTACCA 276
Qy      41 CysArgPheThrLeuGlyProgluAspGlnGlyProLeuAsp1leglulThLeuSer 60
Db      277 TGCAGATTACTCTCAGCTCCCGAAGACAGGAGACCACTGACATTTGAATGCTGATATCC 336
Qy      61 ProAlaAspAsnGlnysValaAspGlnVal1lelleuTySerGlyAsp1ys1leTy 80
Db      337 CCTCTGATTAACAGATAGTGATCAAGTATATTTGATTTCTGGAGCAAAATTTAT 396
Qy      81 AspAspTyTyTyGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
Db      397 GATTACTACTATCCGATCTGAAAGACGGGTACATTTTCAGATACGATGTCAGTCT 456
Qy      101 GlyAspAlaSer1leAsnVal1ThrAsnLeuGlnLeuSerAsp1leglulThTyGlnCys 120
Db      457 GGGAGCGCATCTATAATGATGACCAACCTGACGCTGCGACATTGGCACTTACCAAGTGC 516
Qy      121 LysVal1ylsValaProgl1yVal1GlyAsnLys1leGlnLeuThrVal1leuLys 140
Db      517 AAAGTGAAAGAACCCCTGGGGGTGGCAAAATAGAAATTCCTGCTGACCGCTTGTTAAG 576

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```
QY 141 ProSerGlyThyArgCysTyrValAspGlySerGluGluIleGlyAsnAspPheLysLeu 160
Db 577 CCTTCAGGTACCAAGATGCTTCGGATGATCGGAAGAGATTGGAATGACTTCAAGCTA 636
QY 161 LysCysGluProLysGluGlySerLeuProLeuLeuTyrGluTyrPglLysLeuSerAsn 180
Db 637 AAATGTGAACCCAAAGGAGGCTCCCTTCCACTACAGTTTAAATGGCGAAACGTGCGAC 696
QY 181 SerGlnLysLeuProThrLeuThrLeuValLeuIleGlyLeuIleIlePheCysCys 200
Db 697 TCCCAAGACATGCTTACGCGCATGGCTGGCGAAATGACGTCACAGTTATATCTGTGAAG 756
QY 201 AsnAlaSerThrGluTyrSerGlyTyrThrTyrSerCysThrValLysAsnArgValGlySer 220
Db 757 AACGCCAGTCTGATGATCTCTGGGACATACAGCTGCACGGTTCAAAACAGAGTGGGCTCT 816
QY 221 AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIleAla 240
Db 817 GACCAAGTATGCTGCGACTAGACGTTGTCCACCCCTCCAAACCGAGCCGGAACGATCGCG 876
QY 241 GlyAlaValIleGlyValLeuLeuAlaLeuValLeuIleGlyLeuIleIlePheCysCys 260
Db 877 GGGCGCTCATAGGAGCGCTGCTGGCCCTTGTCTCATTCGGGCGCATCTCTTCTGTGT 936

RESULT 15
AAV72025
ID AAV72025 standard; DNA; 795 BP.
XX
AC AAV72025;
XX
DT 29-MAR-1999 (first entry)
XX
DE Adenovirus PACTSG2-SCAR DNA.
XX
KM PACTSG2-SCAR; chimeric protein; adenoviral fibre protein; monomer;
KW trimerisation domain; affinity; substrate; gene therapy vector;
XX attachment; interaction assay; infection; ss.
XX Mastadenovirus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 1..795
FT /*tag= a
FT /product= "PACTSG2-SCAR"
FT /note= "chimeric protein"
XX
PN MO9854346-A1.
XX
PD 03-DEC-1998.
XX
PF 28-MAY-1998; 98MO-US11024.
XX
PR 16-JAN-1998; 98US-0071668.
XX 28-MAY-1997; 97US-0047849.
XX
PA (GENV-) GENVEC INC.
XX
PI Brough DE, Einfeld D, Kovesi I, Lizonova A, Roelink PW,
PI Wickham TJ, Yonehiro G;
XX
DR WPI; 1999-059848/05.
XX
DR P-PSDB; AAW82729.
XX
PT New adenoviral fibre trimer with reduced binding to native substrate
XX ecotopic infection for in vitro applications
XX
PS Example 8; Page 58-59; 103pp; English.
CC This sequence encodes a novel adenovirus chimeric protein, PACTSG2-SCAR.
CC This protein is used in a method for the construction of novel monomers
```

CC having an N-terminus of an adenoviral fibre protein and a trimerisation
CC domain. Such monomers have lower affinity for native substrate than the
CC native adenoviral fibre trimer. Cell lines containing such monomers are
CC used (i) to propagate adenovirus for use as gene therapy vectors (for in
CC vitro or in vivo applications, (ii) as reagents for studying adenoviral
CC attachment and infection, and (iii) in receptor-ligand interaction
CC assays. The new viruses produce minimal ectopic infection (they can not
CC infect native host cells) so are safer as vectors and can be engineered
CC for selective targeting to other cells.

SO Sequence 795 BP; 236 A; 157 C; 191 G; 211 T; 0 other;

Alignment Scores:

Pred. No.:	2,67e-113	Length:	795
Score:	1142.00	Matches:	214
Percent Similarity:	94.63%	Conservative:	15
Best Local Similarity:	86.43%	Mismatches:	13
Query Match:	84.03%	Indels:	0
DB:	20	Gaps:	0

US-09-899-634c-2 (1-261) x AAV72025 (1-795)

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Db 1 ATGGCGCTCTCTGCTGCTTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
QY 21 SerIleThrThrProGluGlnMetIleGluLysAlaLysGlyGluThrAlaTyrLeuPro 40
Db 61 AGTATCACTACTCTCTAAGAGATGATGTAAGAAAGCCAAAGGGAACTGCTATCTGCGC 120
QY 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluTyrLeuLeuSer 60
Db 121 TGCAAATTTACGCTGTAGTCCCGAAGACAGGAGCCGCTGACATCAGTGGCTGATATCA 180
QY 61 ProAlaAspAsnGlnLysValAspGlnValIleIleLeuTyrSerLysAspLysIleTyr 80
Db 181 CCAGCTGAATATCAGAGAGGTGATCAAGATTAATTTATTTCTGAGACAAATTTAT 240
QY 81 AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
Db 241 GATGACTACTATCCAGATCTGAAAGGCCAGTACATTTATCAGATATGATCTCAATCT 300
QY 101 GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys 120
Db 301 GGTGATGATCAATATAATGTAACGAATTTACAACTGTCAGATTTGGCACATATCATGTC 360
QY 121 LysValLysLysAlaProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLeuLys 140
Db 361 AAAGTGAAAAAGAGCTCTGCTGTTGCCAAATTAAGAAATTCATCTGTTAGTAAAG 420
QY 141 ProSerGlyThyArgCysTyrValAspGlySerGluGluIleGlyAsnAspPheLysLeu 160
Db 421 CCTTCAGGTGCGAGATGTTACGTTGATGATCTGAAAGAAATGGAGTGCCTTTAAGAT 480
QY 161 LysCysGluProLysGluGlySerLeuProLeuLeuTyrGluTyrPglLysLeuSerAsn 180
Db 481 AAATGTGAACCAAAAGAGTTCATCTTCATTAAGATGAGTGCAGAAATATGCTGCAC 540
QY 181 SerGlnLysLeuProThrLeuThrLeuValLeuIleGlyLeuIleIlePheCysCys 200
Db 541 TCACAGAAATAGCCCTTCATGTTAGTACGAAATACCTTCTTATATCTGTAAAAA 600
QY 201 AsnAlaSerThrGluTyrSerGlyTyrThrTyrSerCysThrValLysAsnArgValGlySer 220
Db 601 AATGCTCTTCTGAGTACTTGGGACATACAGCTGACGTCGAAACAGAGTGGGCTCT 660
QY 221 AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIleAla 240
Db 661 GATCAGTGCCTGTTGGTCTAAACGTTGTCCCTTCAATTAACAGCTGATCTGATCC 720
QY 241 GlyAla 242
Db 721 GGCTCA 726
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Wed Jul 16 14:24:18 2003

us-09-899-634c-2.rng

Page 16

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Job time : 194 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)
1778.725 Million cell updates/sec

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Perfect score: 1359
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	1224	90.1	1095	4 US-08-928-383-3	Sequence 3, Appl1
3	1224	90.1	1584	4 US-08-928-383-1	Sequence 1, Appl1
4	1216	89.5	1515	4 US-08-928-383-25	Sequence 25, Appl1
5	351.5	25.9	960	4 US-08-597-4958-23	Sequence 23, Appl1
6	351.5	25.9	960	4 US-09-068-051A-23	Sequence 23, Appl1
7	351.5	25.9	2565	4 US-08-597-4958-29	Sequence 29, Appl1
8	351.5	25.9	2565	4 US-09-068-051A-31	Sequence 31, Appl1
9	351.5	25.9	2793	4 US-09-336-536-68	Sequence 68, Appl1
10	351.5	25.9	2803	4 US-09-068-051A-33	Sequence 33, Appl1
11	301.5	22.2	2184	4 US-09-484-970B-161	Sequence 161, Appl1
12	258	19.0	2166	4 US-09-175-928-1	Sequence 1, Appl1

13	246.5	18.1	1182	4 US-09-336-536-38	Sequence 38, Appl1
14	246.5	18.1	1846	4 US-09-336-536-37	Sequence 37, Appl1
15	217	16.0	1387	2 US-08-979-424-2	Sequence 2, Appl1
16	202	14.9	1831	4 US-09-484-970B-84	Sequence 84, Appl1
17	196	14.4	1140	4 US-09-462-270-1	Sequence 1, Appl1
18	196	14.4	1421	3 US-09-188-930-254	Sequence 254, Appl1
19	191	14.1	1421	3 US-09-188-930-70	Sequence 70, Appl1
20	190	14.0	1110	4 US-09-336-536-27	Sequence 27, Appl1
21	190	14.0	1869	4 US-09-336-536-26	Sequence 26, Appl1
22	181.5	13.4	1295	4 US-09-254-465A-8	Sequence 8, Appl1
23	178.5	13.1	1022	4 US-09-152-060-35	Sequence 35, Appl1
24	163.5	12.0	1744	4 US-09-484-970B-83	Sequence 83, Appl1
25	163.5	12.0	2181	4 US-09-254-465A-7	Sequence 7, Appl1
26	163.5	12.0	2181	4 US-09-254-465A-11	Sequence 11, Appl1
27	158	11.6	752	4 US-09-430-503-19	Sequence 19, Appl1
28	158	11.6	752	4 US-09-430-503-23	Sequence 23, Appl1
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34	155	11.4	1151	4 US-09-430-503-7	Sequence 7, Appl1
35	154	11.3	921	2 US-08-184-009-202	Sequence 202, Appl1
36	154	11.3	921	2 US-08-458-356-202	Sequence 202, Appl1
37	154	11.3	921	2 US-08-460-735-202	Sequence 202, Appl1
38	153	11.3	1151	4 US-09-430-503-1	Sequence 1, Appl1
39	149	11.0	1716	2 US-08-147-772-3	Sequence 3, Appl1
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42	149	11.0	1716	3 US-08-153-262-3	Sequence 3, Appl1
43	149	11.0	1716	3 US-08-479-744A-30	Sequence 30, Appl1
44	149	11.0	1716	3 US-08-280-757B-10	Sequence 30, Appl1
45	149	11.0	1716	3 US-09-159-135-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-272-496-1
; Sequence 1, Application US/09272496
; Patent No. 6245966
; GENERAL INFORMATION:
; APPLICANT: Degrexi, James
; TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
; FILE REFERENCE: 90-98
; CURRENT APPLICATION NUMBER: US/09/272,496
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: US 60/092782
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2434
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (60)..(1154)
US-09-272-496-1

Alignment Scores:

Pred. No.: 7.3e-144
Score: 1238.00
Percent Similarity: 94.25%
Best Local Similarity: 89.27%
Query Match: 91.10%
DB: 4
Length: 2434
Matches: 233
Conservative: 13
Indels: 15
Gaps: 0

US-09-899-634c-2 (1-261) x US-09-272-496-1 (1-2434)

QY 1 MetAlaLeuLeuLeuCyGpHeValLeuLeuCyGylValAlaAspLeuThraArgSerLeu 20
DB 60 ATGGCGCTCTGCTGCTTCCGTCGTCGAGTAGTGAGATTCCGCCAGAGATTG 119

```

QY 21 Ser11eThrThrProGluGlnMet11eGluValAlaValSerGluThrAlaTyrLeuPro 40
DB 120 AGTATCACTACTCTCTGTAAGAGATGATGAAAGCCAAAGGGGAAATGCTTATCTGCCG 179
QY 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAsp11eGluTyrPleuLeuSer 60
DB 180 TGCAAATTATCGCTTAGTCCCGAAGACCAAGGAGCCGCTGACATCGAGTGGCTGATATCA 239
QY 61 ProAlaAspAsnGlnValAspGlnVal11eLeuTyrSerGlyAspLys11eTyr 80
DB 240 CCAGCTGATATACGAAGGTGATCAAGATATATTTATATCTGAGACAAATTTAT 239
QY 81 AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
DB 300 GATGACTACTATCCAGATCTGAAAGGCCGAGTATTTTACGAGTATGATCTCAATCT 359
QY 101 GlyAspAlaSer11eAsnVal1ThrAsnLeuGlnLeuSerAsp11eGlyThrTyrGlnCys 120
DB 360 GGTGATGTCATCAATTAATGTAACCAATTTTCAACTGTCAGATATTTGGCACATATCAAGTGC 419
QY 121 LysValLysValAspProGluValGlyAsnLysLys11eGlnLeuThrValLeuLeuLys 140
DB 420 AAAGTGAAGAAAGCTCTGAGTGTGCAATTAAGAGATTCATCTGAGTATCTTGTTAAG 479
QY 141 ProSerGlyThrArgCysTyrValAspGlySerGluGlu11eGlyAsnAspPheLysLeu 160
DB 480 CTTTCAGGTGCGAGATCTTACGTTGATGATGATCTGAAATAATTTGGAATGACTTTAAGATA 539
QY 161 LysCysGluProLysGluGlySerLeuProLeuLeuTyrGluTyrGlnLysLeuSerAsn 180
DB 540 AAATGTGAACCAAAAGAGGTTCACCTTCATTCAGATATGAGTGGCAAAATTTGCTGCAC 539
QY 181 SerGluLysLeuProThrLeuTyrPleuAlaGluMetThrSerProVal11eSerValLys 200
DB 600 TCAAGAAATATGCCACTTATGATGTTAGCAAAATGACTTCATCTGTTAATCTGTAATA 659
QY 201 AsnAlaSerThrGluTyrSerGlyThrTyrSerCysThrValLysAsnArgValGlySer 220
DB 660 AATGCCCTCTCTGATGATCTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGCTCT 719
QY 221 AspGlnCysLeuLeuAspVal1ProProSerAsnArgAlaGlyThr11eAla 240
DB 720 GATCAGAGCTCTGTTGCTTAAAGCTTCCCTCTTCAATTAAGCTGGAATTAATGCA 779
QY 241 GlyAlaVal11eGlyValLeuLeuAlaLeuValLeu11eGlyLeu11eIlePheCysCys 260
DB 780 GGAAGCAATTAAGGAACTTGTGCTTGTAGCGCTCATGTGCTTATCATCTTTGCTGT 839
QY 261 Arg 261
DB 840 CGT 842

```

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/928,383B
/ FILING DATE: 12-SEP-1997
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US 60/026,100
/ FILING DATE: 13-SEP-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mandragouras, Amy E.
/ REGISTRATION NUMBER: 36,207
/ REFERENCE/DOCKET NUMBER: DFN-020
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 227-7400
/ TELEFAX: (617) 742-4214
/ INFORMATION FOR SEQ. ID NO. 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1095 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1095
/ US-08-928-383B-3

Alignment Scores:
Pred. No.: 1,12e-142 Length: 1095
Score: 1224.00 Matches: 232
Percent Similarity: 93.87% Conservative: 13
Best Local Similarity: 88.89% Mismatches: 16
Query Match: 90.07% Indels: 0
DB: 4 Gaps: 0

US-09-899-634c-2 (1-261) x US-08-928-383B-3 (1-1095)
QY 1 MetAlaLeuLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerLeu 20
DB 1 ATGGCGCTCTGCTGCTGCTTCTGCTCTGCTGCTGCGAGTGGATTTCCGCAGAAATTTG 60
QY 21 Ser11eThrThrProGluGlnMet11eGluValAlaValSerGluThrAlaTyrLeuPro 40
DB 61 AGTATCACTACTCTCTGTAAGAGATGATGAAAGCCAAAGGGGAAATGCTTATCTGCCG 120
QY 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAsp11eGluTyrPleuLeuSer 60
DB 121 TGCAAATTATCGCTTAGTCCCGAAGACCAAGGAGCCGCTGACATTCGAGTGGCTGATATCA 180
QY 61 ProAlaAspAsnGlnValAspGlnVal11eLeuTyrSerGlyAspLys11eTyr 80
DB 181 CCAGCTGATATACGAAGGTGATCAAGTCAATTTATTTATCTGAGACAAATTTAT 240
QY 81 AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
DB 241 GATGACTACTATCCAGATCTGAAAGGCCGAGTATTTTACGAGTATGATCTCAATCT 300
QY 101 GlyAspAlaSer11eAsnVal1ThrAsnLeuGlnLeuSerAsp11eGlyThrTyrGlnCys 120
DB 301 GGTGATGTCATCAATTAATGTAACCAATTTTCAACTGTCAGATATTTGGCACATATCAAGTGC 360
QY 121 LysValLysValAspProGluValGlyAsnLysLys11eGlnLeuThrValLeuLeuLys 140
DB 361 AAAGTGAAGAAAGCTCTGAGTGTGCAATTAAGAGATTCATCTGAGTATCTTGTTAAG 420
QY 141 ProSerGlyThrArgCysTyrValAspGlySerGluGlu11eGlyAsnAspPheLysLeu 160
DB 421 CTTTCAGGTGCGAGATCTTACGTTGATGATCTGAAAGAAATTTGGAATGACTTTAAGATA 480
QY 161 LysCysGluProLysGluGlySerLeuProLeuLeuTyrGluTyrGlnLysLeuSerAsn 180
DB 481 AAATGTGAACCAAAAGAGTTCACCTTCATTAACGATATGAGTGGCAAAATTTGCTGCAC 540

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COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

Oy		181	SergInLysLeuProThrIleuTrpLeuAlaGluMetThrSerProValIleSerValLys	200
Db		541	TCACGAANAATCCCACTTCACTGCATTAGCGAANAATACCTTCACTGTATTACTGTAAAA	600
Oy		201	AsnAlaSerThrGluTrpSerGlyThrTyrserCysThrValLysAsnArgValGlySer	220
Db		601	AATGGCTCTTCTGAGACTCTGGGACATACAGCTGTACAGTCAAGAAACAGAGGGGCTCT	660
Oy		221	AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIleAla	240
Db		661	GATCAGTGCTGTTGGGTCTTAACAAGTTGTGCCCTCTTCANATAAGCTGAGACTTAATTGCA	720
Oy		241	GlyAlaValAlaIleGlyValLeuLeuAlaLeuValLeuIleGlyLeuIleIlePheCysCys	260
Db		721	GSAGCATTAATAGAACTTGTGCTGTCTTAGCGCCTCATTTGTTTATCATCTTTTGCTGT	780
Oy		261	Arg 261	
Db		781	GCT 783	

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RESULT 3
US-08-928-383B-1
; Sequence 1, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Coxsackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928, 383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DPN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1584 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 60..1157
; US-08-928-383B-1

Alignment Scores:
Pred. No.: 2,03e-142 Length: 1584
Score: 1224.00 Matches: 232
Percent Similarity: 93.87% Conservative: 13

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US-09-839-634C-2 (1-261) x US-08-928-383B-1 (1-1584)
Best Local Similarity: 88.89% Mismatches: 1e
Query Match: 90.07% Indels: 0
DB: 4 Gaps: 0

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OY		1	MevlAlaLeuLeuLeuCysPheValLeuLeuCysGlyValAlAspLeuThrArgSerLeu	20
Dd		60	ATGGCGCTTCGTGCTGCTTCCGTCTCTGGAGTGATGGATTGCCACAAATTGG	119
OY		21	SerIleThrTrpProGluGlnMetIleGluValAlaLysGlyGluThraIeTyrLeuPro	40
Dd		120	AGTATCACTACTCCCGAAGAAGATGATTGAAAAAGCCAAGGGGAACCTCATCTGGCCG	179
OY		41	CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluTrpLeuLeuSer	60
Dd		180	TGCAAATTTAGCTTAAGTCCGCAACACCAGGAGCCGCTGGACATCCAGTGGCTGAATCA	239
OY		61	ProAlaAspAsnGlnLysValAspGlnValIleIleLeuTySerGlyAspLysIleTyR	80
Dd		240	CCAGCTGTAATCACAGAGGTGGATCAAGTATTATTATTTCTGGAGACAAAATTTAT	299
OY		81	AspAspTyrrTyrgInAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer	100
Dd		300	GATGACTACTATCCAGATCTGATAAAGCCGAGTACATTTTACAGATATGATCTCAATCT	359
OY		101	GlyAspAlaSerIleAsnValThrLeuLeuGlnLeuSerAspIleGlyThyrrTyrgInCys	120
Dd		360	GGTATGATCAATTAATGAATGAACGAATTTACAACGTCCAGATTTGGCACATATCATGTCC	419
OY		121	LysValLysLysAlaPProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLeuLys	140
Dd		420	AAAGGAAAAAAGCTCCCTGGCTTCCAAATAAGAAATTCACTGGTACTTCTGTAAAG	479
OY		141	ProSerGlyThrArgCysTyrrValAspGlySerGluGlnIleGlyAsnAspPheLysLeu	160
Dd		480	CCTTCAGGTGGAGAGATGTTACGTCATGATGATCTGAAGAAATTTGGAATGATCACTTAAAGA	539
OY		161	LysCysGluPProLysGluGlySerLeuProLeuLeuTyrrGluTrpGlnLysLeuSerAsn	180
Dd		540	AAATGTGAACCAAAGAAAGTTCCACTTCCATTACGTATGATGATGGCAAAAATTTGCTTGAC	599
OY		181	SerGlnLysLeuProThrLeuTrpLeuIagiMetThrSerProValIleSerValLys	200
Dd		600	TCACAGAAAAGCCCACTTCATCGTTAGAGAAAATGACTTCATCTGTATATCTGTAAAA	659
OY		201	AsnAlaSerThrGluTyrrSerGlyThyrrTyrrSerCysThrValLysAsnArgValGlySer	220
Dd		660	AATGCTCTTCTGGATCTCTGGGACATAACACTGTACAGTACAGAAACAGAGGGGCTCT	719
OY		221	AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgIagiTyrrIleAla	240
Dd		720	GATCAGTCCCTGTGCGTCTTAACGTTGTCTCTCTTCAAAATAAACCTGACTAATTGCA	779
OY		241	GlyAlaValIleGlyValLeuLeuAlaLeuValLeuIleGlyLeuIleIlePheCys	260
Dd		780	GGAGGCATTATAGAACTTTGGCTTCTCTACAGGCTCATTTGCTTATCATCTTTTCTGT	839
OY		261	Arg	261
Dd		840	CGT	842

RESULT 4
US-08-928-383B-25
: Sequence 25, Application US/08928383B
: Patent No. 6210921
: GENERAL INFORMATION:
: APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
: APPLICANT: and Marshall S. Horwitz
: TITLE OF INVENTION: CR, A No. 6210921el Cxsackievirus and Adenovirus
: TITLE OF INVENTION: Receptor
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESSES:
:

```

ADDRESSER: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
City: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1515 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1095
US-08-928-383B-25
Alignment Scores:
Pred. No.: 1.87e-141 Length: 1515
Score: 1216.00 Matches: 229
Percent Similarity: 93.85% Conservative: 15
Best Local Similarity: 88.08% Mismatches: 16
Query Match: 89.48% Indels: 0
DB: 4 Gaps: 0
US-09-899-634C-2 (1-261) x US-08-928-383B-25 (1-1515)
QY 1 MetAlaIeuIeuIeuCysPheValIeuIeuCysGlyValAlaAspLeuThrArgSerIeu 20
Db 1 ATGGCGGCGCTACTGCTGCTTCGCGCTTGTGCGGGATGCGCGGATTTCACCAAGTGTTG 60
QY 21 SerIleThrThrProGluInMetIleGluValAlaIysGlyGluThrAlaTyrLeuPro 40
Db 61 AGCATCATTACACCCGACAGAGGATCGAAAAAGCCAAAGGGAAACCTGCTATTACCA 120
QY 41 CysArgPheThrIeuGlyProGluAspGlnGlyProLeuAspIleGluTyrLeuIeuSer 60
Db 121 TGGCAAGTTTACTCTCAGTCCCGCAAGACCAAGGACCACTGACATTGAGTGCATATCC 180
QY 61 ProAlaAspAsnGlnIysValAspGlnValIleIleLeuTyrSerGlyAspValIleTyr 80
Db 181 CCGCTCGATACCAAGATAGTGAATCAAGATCATTTGTATTTGAGAACAAATTTAT 240
QY 81 AspAspTyrTyrGlnAspLeuIysGlyArgValIHisPheThrSerAsnAspLeuIysSer 100
Db 241 GATTACTACTATCCGATCTGGAAGACCGGGTACATTTTACAGATACGATGTCAAGCT 300
QY 101 GlyAspAlaSerIleAsnValThrAsnIeuGlnIeuSerAspIleGlyThrTyrGlnCys 120
Db 301 GCGCAGCCATCTTAATATGTGACCAACCTGCAGCTGTGCGACATTGGCATTCACAGTGC 360
QY 121 LysValIysIysAlaProGlyValGlyAsnIysIysIleGlnLeuThrValLeuLeuIys 140
Db 140

```

Db 361 A A A T G A A G A A A G C C C T G G G G T T G C A A A T A G A A A A T T C T G C T G A C C G T T C T G T T A A G 420

Qy 141 P r o s e r g l y t h r a g c y s t y r v a l a s p g l y s e r g l u g l i e g l y a s a s p h e l y s l e u 160

Db 421 C C T T C A G A G T A C A A A T G C T T G T G T A T G A T C G G A A G A G A T T G A A A T G A C T T C A A G T A 480

Qy 161 L y s C y s g l u p p o l y s g l u g l y s e r l e u p r o b e u l e u t y r g l u t r p g l n l y s e u s e r a e n 180

Db 481 A A A T G T A A C C C A A G A A G A G C T C C C T T C A C T A C A G T T G A A T G G C A G A A A C T G T C G A C 540

Qy 181 S e r g l n l y s l e u p r o t h r l e u t r p l e u a l a g l u e t h r s e r p r o v a l l e s e r v a l l y s 200

Db 541 T C C C A G A C A A T G C T C A C C C A T G C T G C A G A A A T G A C G T C A C C A G T T A T A T C T G T G A A G 600

Qy 201 A s n a l a s e r t h r g l u t y r s e r g l y t h r y s e r c y s t h r v a l l y s a s n a r y a l g l y s e r 220

Db 601 A A C C C A G T T C T G A T A T T C T G G A C A T A C A G C T G C A C G T T C A A A A C A G A C T G G G C T C T 660

Qy 221 A s p g l n c y s l e u l e u a r g l e u a s p v a l a p r o p r o s e r a s n a r a l a g l y t h r l e a l a 240

Db 661 G A C C A G T A T G C T G C G A C T A G A G T G T C C A C C T C A A C G A G C G G A A C G A T C G G 720

Qy 241 G l y a l a v a l l e g l y a l l e u l e u a l a e u v a l l e u l l e g l y l e u l l e i l e p h e y c y s 260

Db 721 G G C C C C C T C A T A G G A G A C G C T C T G C C C T T G T G C T C A T C G G G C C A T C C T C T T C T G C T 780

RESULT 5

US-08-597-495B-23

Sequence 23, Application US/08597495B

Patent No. 5712369

GENERAL INFORMATION:

APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;

APPLICANT: Simpson, Richard U.; Nice, Edouard; Moritz, R. L.;

APPLICANT: Catmel, B.; Ji, Hong; Burgess, Anthony W.;

APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron

TITLE OF INVENTION: Colon Cell And Colon Cancer Cell

TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felte & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/597,495B

FILING DATE: 02-Feb-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/511,876

FILING DATE: 04-Aug-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5712369man D.

REGISTRATION NUMBER: 30,946

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 960 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-597-495B-23

Alignment Scores:

Pred. No.: 3,39e-34 Length: 960
 Score: 351.50 Matches: 89
 Percent Similarity: 54.41% Conservative: 53
 Best Local Similarity: 34.10% Mismatches: 96
 Query Match: 25.86% Indels: 23
 DB: 1 Gaps: 11

US-09-899-634c-2 (1-261) x US-09-597-495B-23 (1-960)

QY 10 LeuCyGgIyValAlaAspLeuThrArgSerLeuSerIleThrThProGluGlnMetIle 29
 |||||
 Db 34 CTCTGTGCAGTCAGGGTGAACCGTCGATGCCATCTCTGTGAAACTCCGACGACGCTTCT 93
 |||||
 QY 30 GluLyAlaIyGgIyGluThralaTyLeuProCyAspPheThrLeuGlyProGluAsp 49
 |||||
 Db 94 CGGGCTTCGAGGGAAGAGTGCACCTGCGCTGCACCTACACACTTCACCTCCAGT 153
 |||||
 QY 50 GlnGlyProLeuAspIleGluTrp-----LeuLeuSerProAlaAspAnglnLys 66
 |||||
 Db 154 CGAGAGGAGCTT---ATTCAATGGATTAAGCTCTCTCACT-----CAT 195
 |||||
 QY 67 ValAspGlnValIleIleLeuTySerGlyAspLys-----IleTyAspAspTyTr 84
 |||||
 Db 196 ACGGAAGGGTGTCTATCTGGCCGTTTCAAAACAACTACATCCATGCTGAGCTTAT 255
 |||||
 QY 85 GlnAspLeuLyGgIyArgValHisPheThrSerAsnAspLeuLySerGlyAspAlaSer 104
 |||||
 Db 256 -----AAGATGCGCTCAGACATA---TCCAAACAATGCTGAGAGTCCGATGCTCC 303
 |||||
 QY 105 IleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyGlnCysLysValLysLys 124
 |||||
 Db 304 ATCACCATTGATCAGTGCACCAAGCTGACCAAGGACCTACAGAGTTCGTCTGCTG 363
 |||||
 QY 125 AlaProGlyVal---GlyAsnLysLys-----IleGlnLeuThrValLeuLeuLysPro 141
 |||||
 Db 364 ATGTGACACTGAGAGGCAACACCAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 423
 |||||
 QY 142 SerGlyThrArgCysTyTrValAspGlySerGluGluIleGlyAsnAspPheLysLys 161
 |||||
 Db 424 TCCAAACCAAGATGCGCATCGAGGAGAGACCATTAATGGGAACAATCCAGCTGACC 483
 |||||
 QY 162 CysGluProLyGgIyGluTySerLeuProLeuLeuTyGluTrpGlnLysLeuSer---Asn 180
 |||||
 Db 484 TGCATCAACAAAGAGGGCTCACCAACCTCAGTACAGCTGGAAGAGGATCAACATCTCG 543
 |||||
 QY 181 SerGlnLysLeuProThrLeuTrpLeuAlaGlnMetThrSer---ProValIleSerVal 199
 |||||
 Db 544 AATCAGGAGAGCC-----CTGGCCCAAGCCCTCAGCTCAGCTGCTCTCCCTG 594
 |||||
 QY 200 LysAsnAlaSerThrGluTySerGlyThrTySerCysThrValLysAsnArgValGly 219
 |||||
 Db 595 AAGAAATATCTCCACACACATCGGGTTACTACTGATCTGATCCCAAGCAATAGAGGGG 654
 |||||
 QY 220 SerAspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIle 239
 |||||
 Db 655 ACGCACTTGTCAACATCAACGCGGTGCGTCAAGATCTCCCTCCATGAAGCTGGCCCTGAT 714
 |||||
 QY 240 AlaGlyAlaValIleGlyValLeuLeuAlaLeuValLeuIleGlyLeuIleIlePheCys 259
 |||||
 Db 715 GTGGGATCGCGGTGGCGGTGTGTCAGCCCTCATTAATATGGAATCAATCAATCACTAC 774
 |||||
 QY 260 Cys 260
 |||||
 Db 775 TGC 777

RESULT 6

US-09-068-051A-23
 ; Sequence 23, Application US/09068051A
 ; Patent No. 6291235

GENERAL INFORMATION:

APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
 Simpson, Richard J.; Nice, Eduard; Moritz, R. L.;
 Catimel, B.; Ji, Hong; Burgess, Anthony W.;

Heath, Joan K.; White, Sara J.; Johnstone, Cameron
 TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
 Associated Nucleic Acid Molecules, Protein And Peptides
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESS: Fulbright & Jaworski LLP
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10103

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 360 Kb storage

COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/068,051A

FILING DATE: 10-Dec-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/597,495

FILING DATE: 02-Feb-1996

APPLICATION NUMBER: 08/511,876

FILING DATE: 04-Aug-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6291235man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5316.2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3168

TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 23

SEQUENCE CHARACTERISTICS:

LENGTH: 960 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 23

US-09-068-051A-23

Alignment Scores:
 Pred. No.: 3,39e-34 Length: 960
 Score: 351.50 Matches: 89
 Percent Similarity: 54.41% Conservative: 53
 Best Local Similarity: 34.10% Mismatches: 96
 Query Match: 25.86% Indels: 23
 DB: 4 Gaps: 11

US-09-899-634c-2 (1-261) x US-09-068-051A-23 (1-960)

QY 10 LeuCyGgIyValAlaAspLeuThrArgSerLeuSerIleThrThProGluGlnMetIle 29
 |||||
 Db 34 CTCTGTGCAGTCAGGGTGAACCGTCGATGCCATCTCTGTGAAACTCCGACGACGCTTCT 93
 |||||
 QY 30 GluLyAlaIyGgIyGluThralaTyLeuProCyAspPheThrLeuGlyProGluAsp 49
 |||||
 Db 94 CGGGCTTCGAGGGAAGAGTGCACCTGCGCTGCACCTACACACTTCACCTCCAGT 153
 |||||
 QY 50 GlnGlyProLeuAspIleGluTrp-----LeuLeuSerProAlaAspAnglnLys 66
 |||||
 Db 154 CGAGAGGAGCTT---ATTCAATGGATTAAGCTCTCTCACT-----CAT 195
 |||||
 QY 67 ValAspGlnValIleIleLeuTySerGlyAspLys-----IleTyAspAspTyTr 84
 |||||
 Db 196 ACGGAAGGGTGTCTATCTGGCCGTTTCAAAACAACTACATCCATGCTGAGCTTAT 255
 |||||
 QY 85 GlnAspLeuLyGgIyArgValHisPheThrSerAsnAspLeuLySerGlyAspAlaSer 104
 |||||
 Db 256 -----AAGATGCGCTCAGACATA---TCCAAACAATGCTGAGAGTCCGATGCTCC 303
 |||||
 QY 105 IleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyGlnCysLysValLysLys 124
 |||||

DB 304 ATCACCATTGATGCTGACCTGCTGCTGACACGCGACCTACGAGTCTTCTGCTGCTG 363
QY 125 AlaProGlyVal---GlyAsnLysLys-----IleGlnLeuThrValLeuLeuLysPro 141
DB 364 ATGTCAGACCTGGAGGGGACACCAAGTCACTGCTCGCTGTTGGTCTCTGTCGCCACC 423
QY 142 SerGlyThrArgCysTyrValAspGlySerGluGluIleGlyAsnAspPheLysLys 161
DB 424 TCCAAACCAAGATGCGGCATCGAGGGAGAGACCATTAATTGGAAACAACATCCAGCTGACC 483
QY 162 CysGluProLysGluGlySerLeuProLeuLeuTyrGluTyrGlnLysLeuSer---Asn 180
DB 484 TGCCAATCAAAAGAGGGCTCCACCAACCCCTCAGTACAGCTGGAAGAGTCAACATCTCTG 543
QY 181 SerGluLysLeuProThrLeuTyrLeuAlaGluMetThrSer---ProValIleSerVal 199
DB 544 AATCAGAGAGAGAGCC-----CTGGCCAGCGACCTCAGCTCAGCTGCTCTCTG 594
QY 200 LysAsnAlaSerThrGluTyrSerGlyThrTyrSerCysThrValLysAsnArgValGly 219
DB 595 AAGAAATATCTCCACAGACATCGGGTTACTATCATCTGTACCTCCAGCATGAGAGGGG 654
QY 220 SerAspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIle 239
DB 655 ACCCAGTCTTGCACATCATCGGTGGCCGCTGAGATCTCTCCATGAACTGAGCCCTGTAT 714
QY 240 AlaGlyAlaValIleGlyValLeuLeuAlaLeuValLeuIleGlyLeuIleIlePheCys 259
DB 715 GTGGGATCGCGGTGGGTGGTTCAGACCTCATTAATGACATCATCATCTACTGTC 774
QY 260 Cys 260
DB 775 TGC 777

RESULT 7
US-08-597-495B-29
; Sequence 29, Application US/08597495B
; Patent No. 571369
; GENERAL INFORMATION:
; APPLICANT: Old, Lloyd J.; Welt, Sydney; Rittner, Gerd;
; APPLICANT: Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
; APPLICANT: Catmel, B.; Ji, Hong; Burgess, Anthony W.;
; APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron
; TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
; TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/597,495B
; FILING DATE: 02-Feb-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/511,876
; FILING DATE: 04-Aug-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5712369man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5316.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 29:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2565 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-597-495B-29

Alignment Scores:
Pred. No.: 1,64e-33 Length: 2565
Score: 351.50 Matches: 89
Percent Similarity: 54.41% Conservative: 53
Best Local Similarity: 34.10% Mismatches: 96
Query Match: 25.86% Indels: 23
DB: 1 Gaps: 11

US-09-899-634c-2 (1-261) x US-08-597-495B-29 (1-2565)

QY 10 LeuCysGlyValAlaAspLeuThrArgSerLeuSerIleThrThrProGluGlnMetIle 29
DB 146 CTCCTGTGACAGTCAAGGAGTACCGTCATGTCATCTCTGTGAAACCTCCGAGAGCGTTCTT 205
QY 30 GlnLysAlaLysGlyValThrAlaTyrLeuProCysArgPheThrLeuGlyProGluAsp 49
DB 206 CGGGCTTGCAGGAGAAAGGTGTACCTGCTGACCTGACCTACCACTTCACCTCCAGT 265
QY 50 GlnGlyProLeuAspIleGluTyrP-----LeuLeuSerProAlaAspAsnGlnLys 66
DB 266 CGAGAGGAGACTT---ATTCAATGGATTAAGCTCTCTCTACT-----CAT 307
QY 67 ValAspGlnValIleLeuLeuTyrSerGlyAspLys-----IleTyrAspAspTyrTyr 84
DB 308 ACCGAAAGGTGGTGTATCTGGCCGTTTTCACAAACAAACTACATCATCATGAGCTTTAT 367
QY 85 GlnAspLeuLysGlyValArgValHisPheThrSerAsnAspLeuLysSerGlyAspAlaSer 104
DB 368 -----AAGAAATGCGTCAGACATA---TCCAAACAATGTCGAGATGCCAGTCTCC 415
QY 105 IleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCysLysValLysLys 124
DB 416 ATCACCATTGATCAGCTGACATGACGCTGACACACGACCTACGAGTCTCTGCTGCGG 475
QY 125 AlaProGlyVal---GlyAsnLysLys-----IleGlnLeuThrValLeuLeuLysPro 141
DB 476 ATGTCAGACCTGGAGGGCAACCAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 535
QY 142 SerGlyThrArgCysTyrValAspGlySerGluGluIleGlyAsnAspPheLysLys 161
DB 536 TCCAAACCAAGATGCGGCATCGAGGGAGAGACCATTAATTGGAAACAATCCAGCTGACC 595
QY 162 CysGluProLysGluGlySerLeuProLeuLeuTyrGluTyrGlnLysLeuSer---Asn 180
DB 596 TGCCAATCAAAAGAGGGCTCCACCAACCTCAGTACAGCTGGAAGAGTGAACAACATCTG 655
QY 181 SerGluLysLeuProThrLeuTyrLeuAlaGluMetThrSer---ProValIleSerVal 199
DB 656 AATCAGAGAGAGAGCC-----CTGGCCAGCGACCTCAGCTCAGCTGCTGCTCTG 706
QY 200 LysAsnAlaSerThrGluTyrSerGlyThrTyrSerCysThrValLysAsnArgValGly 219
DB 707 AAGAAATATCTCCACAGACATCGGGTTACTATCATCTGTACCTCCAGCATGAGAGGGG 766
QY 220 SerAspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIle 239
DB 767 ACCCAGTCTTGCACATCATCGGTGGCCGCTCAGATCTCTCTCCATGAACTGAGCCCTGTAT 826
QY 240 AlaGlyAlaValIleGlyValLeuLeuAlaLeuValLeuIleGlyLeuIleIlePheCys 259
DB 827 GTGGGATCGCGGTGGGTGGTTCAGACCTCATTAATGATGATGATGATCATCATCTACTGC 886
QY 260 Cys 260
DB 887 TGC 889

RESULT 8
US-09-068-051A-31
Sequence 31, Application US/09068051A
Patent No. 6291235
GENERAL INFORMATION:
APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
Cattell, B.; Ji, Hong; Burgess, Anthony W.;
Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
Associated Nucleic Acid Molecules, Protein and Peptides
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,051A
FILING DATE: 10-Dec-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597,495
FILING DATE: 02-Feb-1996
APPLICATION NUMBER: 08/511,876
FILING DATE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6291235man D.
REGISTRATION NUMBER: 30,946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 31
SEQUENCE CHARACTERISTICS:
LENGTH: 2565 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31
US-09-068-051A-31
Alignment Scores:
Pred. No.: 1,64e-33 Length: 2565
Score: 351.50 Matches: 89
Percent Similarity: 54.41% Conservative: 53
Best Local Similarity: 34.10% Mismatches: 96
Query Match: 25.86% Indels: 23
DB: Gaps: 11
US-09-899-634c-2 (1-261) x US-09-068-051A-31 (1-2565)
QY 10 LeuCyGlyValAlaAspLeuThrArgSerLeuSerIleThrThrProGluGlnMetIle 29
DB 146 CTCGTGACGTGACGGTGCACCGTCGATGCATCTCTGTGAACTCCGACGAGCGTTCTT 205
QY 30 GluValAlaIleGlyGlnThrAlaIleThrLeuProCysArgPheThrIleGluGlyProGluAsp 49
DB 206 CGGAGCTTCGAGGAGAAAGAGTGCACCTGCGCTGCACCTACACACTTCACCTCCAGT 265
QY 50 GlnGlyProLeuAspIleGluTrp-----LeuLeuSerProAlaAspGlnIle 66
DB 266 CGAGAGGAGCTT---ATTCAATGAGATAACTCTCTCTACT-----CAT 307
QY 67 ValAspGlnValIleIleLeuTyrsGlyAspLys-----IleTyrsAspTyTy 84

DB 308 ACCGAAAGGGTGTCTATCTGCCCTTTTCAAAACAAAACCTACATCATGCTGACTTAT 367
QY 85 GlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSerGlyAspAlaSer 104
DB 368 -----AAGATTCGCTCAGCAT---TCCACAAATGCTGAGACAGTCCAGTCTCC 415
QY 105 IleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrGlnCysLysValLysLys 124
DB 416 ATCACCATTGAATCAGCTGACCTGACCTGCAACAGGACCTACAGAGTGTCTCTGCTG 475
QY 125 AlaProGlyVal---GlyAsnLysLys-----IleGlnLeuThrValLeuLeuLysPro 141
DB 476 ATGTACAGCTTGAGGAGCAACACCAATGACCTGCTGCTGTGTCTCTGCGCACCC 535
QY 142 SerGlyThrArgCysTyrsValAspGlySerGluGlnIleGlyAsnAspPheLysLys 161
DB 536 TCCAAACCAAGATGCGGCTCAGAGGAGAGACCATTAATTGGGAACAACATCCAGCTGACC 595
QY 162 CysGluProLysGlnGlySerLeuProLeuLeuTyrsGluTrpGlnLysLeuSer---Asn 180
DB 596 TGCATATCAAGAGAGGCTCACCAACCTCAGTACAGCTGGAAGAGTAACAACATCTCG 655
QY 181 SerGlnLysLeuProThrLeuThrLeuAlaGluMetThrSer---ProValIleSerVal 199
DB 656 AATCAGAGACGACCC-----CTGGCCACGACGCTCAGTACGCTGTCTCTCTG 706
QY 200 LysAsnAlaSerThrGluTyrsSerGlyThrTyrsCysThrValLysAsnArgValGly 219
DB 707 AAGATATCTCCACAGACATCGGCTTACTGACTGTAACCTCCAGCAATGAGAGGGG 766
QY 220 SerAspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIle 239
DB 767 ACGCAGTTCGCAACATCAGCGTGGCGGTGACATCTCCATGAACTGGGCGCTGTAT 826
QY 240 AlaGlyAlaValIleGlyValLeuLeuAlaLeuValIleGlyLeuIleIlePheCys 259
DB 827 GTGGCGATCGCGTGGCGGTGTTCAGCCCTCATATCATGAGCATCATCTACTATCG 886
QY 260 Cys 260
DB 887 TGC 889
RESULT 9
US-09-336-536-68
Sequence 68, Application US/09336536
Patent No. 6406864
GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 68
LENGTH: 2793
TYPE: DNA
ORGANISM: Homo sapiens
US-09-336-536-68
Alignment Scores:
Pred. No.: 1,88e-33 Length: 2793
Score: 351.50 Matches: 89
Percent Similarity: 54.41% Conservative: 53
Best Local Similarity: 34.10% Mismatches: 96
Query Match: 25.86% Indels: 23
DB: Gaps: 11
US-09-899-634c-2 (1-261) x US-09-336-536-68 (1-2793)
QY 10 LeuCyGlyValAlaAspLeuThrArgSerLeuSerIleThrThrProGluGlnMetIle 29

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|||||
378 CTCTGTGACGTGAGGGTGAACCTGATGACCATCTGTGTGAAACTCCGAGGAGCTTCTT 437
QY 30 GtLysAlaLysGlyGlnThrAlaTyrLeuProCysArgPheThrLeuGlyProGluAsp 49
Db 438 CGGGCTTCGAGGAGGAGGTGACCTGCTGACCTTACCACTTCCACCTCCACCTCCAGT 497
QY 50 GlnGlyProLeuAspIleGluTrp-----LeuLeuSerProAlaAspAsnGlnLys 66
Db 498 CGAGAGGAGCTT---ATTCAATGGAGTAAGTCTCTCTCACT-----CAT 539
QY 67 ValAspGlnValIleIleLeuTyrSerGlyAspLys-----IleTyrAspAspTyrTyr 84
Db 540 ACCGAAAGGCTGGCATCTGCGCTTTTCAACAAAATACTACATCCATGCTGAGCTTTAT 599
QY 85 GlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSerGlyAspAlaSer 104
Db 600 -----AAGATTCGCGTACAGATA---TCCAAACATGCTGAGCATCCGATGCTCC 647
QY 105 IleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCysLysValLysLys 124
Db 648 ATACACCATGATGATGACCATGACCATGCTGACAGGACCTTACGAGTCTTCTGCTGCTG 707
QY 125 AlaProGlyVal---GlyAsnLysLys-----IleGlnLeuThrValLeuLeuLysPro 141
Db 708 ATGTCAACCTGAGGAGGCAACACCACTCACTGTCTGCTGCTGCTGCTGCTGCTGCTG 767
QY 142 SerGlyThrArgCysTyrValAspGlySerGlnGluIleGlyAsnAspPheLysLys 161
Db 768 TCCAAACCAAGATGCGGATCGAGGAGAGACCACTTAATGGAAACAATCCAGCTGAC 827
QY 162 CysGluProLysGlnGlySerLeuProLeuLeuTyrGlnLysLeuSer---Asn 180
Db 828 TGCCAATCAAGAGGAGGCTCACCACCCCTCAGTACAGCTGGAAGAGTACCAATCCTG 887
QY 181 SerGlnLysLeuProThrLeuTyrPheLeuAlaGluMetThrSer---ProValIleSerVal 199
Db 888 AATCAGAGAGAGCC-----CTGCCAGCAGCAGCTCAGAGTCACTGCTGCTGCTGCTG 938
QY 200 LysAsnAlaSerThrGlnTyrSerGlyThrTyrSerCysThrValLysAsnArgValGly 219
Db 939 AAGATATCTTCCAGACACATCGGCTTACTACTGTAATCTTCCACCAATGAGAGAGG 998
QY 220 SerAspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIle 239
Db 999 ACCGAGTTCGAAACATCAGCGTGGCGCTCAGATCTCCCTCCAGAACGAGCCCTGAT 1058
QY 240 AlaGlyAlaValIleGlyValLeuLeuAlaLeuValLeuIleGlyLeuIleIlePheCys 259
Db 1059 GTGGGATCGCGGTGGCGGTGTGTCAGCCCTCATATTCATTCGATCATCATCTACTGC 1118
QY 260 Cys 260
Db 1119 TGC 1121

RESULT 10
US-09-068-051A-33
; Sequence 33. Application US/09068051A
; Patent No. 6291235
; GENERAL INFORMATION:
; APPLICANT: Old, Lloyd J.; Welt, Sydney; Riteer, Gerd;
; Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
; Catmel, B.; Ji, Hong; Burgess, Anthony W.;
; Heath, Joan K.; White, Sara J.; Johnstone, Cameron
; TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
; Associated Nucleic Acid Molecules, Protein And Peptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA

```

```

; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/068,051A
; FILING DATE: 10-Dec-1998
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/597,495
; FILING DATE: 02-Feb-1996
; APPLICATION NUMBER: 08/511,876
; FILING DATE: 04-Aug-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6291235man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5316.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2803 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-068-051A-33

Alignment Scores:
Pred. No.: 1,89e-33 Length: 2803
Score: 351.50 Matches: 89
Percent Similarity: 54.41% Conservative: 53
Best Local Similarity: 34.10% Mismatches: 96
Query Match: 25.86% Indels: 23
DB: 4 Gaps: 11

US-09-899-634c-2 (1-261) x US-09-068-051A-33 (1-2803)
QY 10 LeuCysGlyValAlaAspLeuThrArgSerLeuSerIleThrThrProGluIleMetIle 29
Db 378 CTCTGTGACGTGAGGGTGAACCTGATGACCATCTGTGTGAAACTCCGAGGAGCTTCTT 437
QY 30 GtLysAlaLysGlyGlnThrAlaTyrLeuProCysArgPheThrLeuGlyProGluAsp 49
Db 438 CGGGCTTCGAGGAGGAGGTGACCTGCTGACCTTACCACTTCCACCTCCACCTCCAGT 497
QY 50 GlnGlyProLeuAspIleGluTrp-----LeuLeuSerProAlaAspAsnGlnLys 66
Db 498 CGAGAGGAGCTT---ATTCAATGGAGTAAGTCTCTCTCACT-----CAT 539
QY 67 ValAspGlnValIleIleLeuTyrSerGlyAspLys-----IleTyrAspAspTyrTyr 84
Db 540 ACCGAAAGGCTGGCATCTGCGCTTTTCAACAAAATACTACATCCATGCTGAGCTTTAT 599
QY 85 GlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSerGlyAspAlaSer 104
Db 600 -----AAGATTCGCGTACAGATA---TCCAAACATGCTGAGCATCCGATGCTCC 647
QY 105 IleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCysLysValLysLys 124
Db 648 ATACACCATGATGATGACCATGACCATGCTGACAGGACCTTACGAGTCTTCTGCTGCTG 707
QY 125 AlaProGlyVal---GlyAsnLysLys-----IleGlnLeuThrValLeuLeuLysPro 141
Db 708 ATGTCAACCTGAGGAGGCAACACCACTCACTGTCTGCTGCTGCTGCTGCTGCTGCTG 767
QY 142 SerGlyThrArgCysTyrValAspGlySerGlnGluIleGlyAsnAspPheLysLys 161
Db 768 TCCAAACCAAGATGCGGATCGAGGAGAGACCACTTAATGGAAACAATCCAGCTGAC 827

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Db      242 ATGAGGCAATTCTATTACTTTTCAGGTGGAGCAAGCTGATGACCATCGGGCAATT 301
Qy      85 GLASP---LeuysgIyArgValHiePheThSerAsnAspleuysSerGIyAspAla 103
Db      302 AAGATGCAATTACAGG-----TCCAACGAT-----CAGGTAATGCA 340
Qy      104 SerLeuAsnValThrAsnLeuGlnLeuSerAspIleGIyThrYrGlnCysLysValLys 123
Db      341 TCATCACTATCTCGCATGACAGCCAGACAGTGAATTATCATCTCGATGTTAAC 400
Qy      124 LysAlaPro-----GlyValGIyAsnLysLysIleGlnLeuThrValLeuLeuLys 140
Db      401 AACCCCCCAAGCTTCTCGGCCAAACCAAGCATCTCAACGTCAGCTGTGTAGTAAA 460
Qy      141 ProSerGIyThrArgCysTyRValAspGIySerGIyGlnIleGlnLeuAsnAspPheLysLeu 160
Db      461 CTTTCAAGCCCTTTGTAGCGTTCAAGGAAGACCAAACTGGCCACACTATTTCCCTT 520
Qy      161 LysCysGlnProLysGlnGIySerLeuProLeuLeuTyRGIyTrpGlnLysLeuSerAsn 180
Db      521 TCCTGTCTCTCGGCTTGGACACCTTCCCTGTGACTGACTGATTAACCTTGAGGA 580
Qy      181 SerGlnLysLeuProThrLeuTrpLeuAlaGlnMetThrSerProValIleSerValLys 200
Db      581 AGAGACATCGTGCAGTGAAGAAACCTCAACCCCAACCCGGGATTTGGTCATTGGA 640
Qy      201 AsnAlaSerThrGlnTyRserGIyThrTyRserCysThrValLysAsnArgValGIySer 220
Db      641 AATGTGCAAAATTTTGAACAAAGTTATTACAGTGTCTGCATCAACAGATGGCAAT 700
Qy      221 AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGIyThrIleAla 240
Db      701 AGTTCCTGTC-----GAATCGATCTCATCTTCCATCCAGAAAGTTGGATATTGTT 754
Qy      241 GIYAlaValIleGIyValLeuLeu---AlaLeuValLeuIleGIyLeuIleIlePhe 258
Db      755 GGGGCTTGATGTGATGCTGTCGTGAGTGGCCGCAATCATCTCTGTGTGTGCTTC 811
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RESULT 13

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US-09-336-536-38
; Sequence 38, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336,536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-336-536-38
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Alignment Scores:

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Pred. No.: 5,51e-21 Length: 1182
Score: 246.50 Matches: 79
Percent Similarity: 47.46% Conservative: 52
Best Local Similarity: 28.62% Mismatches: 108
Query Match: 18.14% Indels: 37
DB: 4 Gaps: 12
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US-09-899-634c-2 (1-261) x US-09-336-536-38 (1-1182)

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Qy      3 LeuLeuLeuCysPheValLeuLeuCysGIyValAlaAspLeuThrArgSer----- 19
Db      37 CTGGGGGTTTGTCTCGGACCTGATGTAACCTTGTCTTCCGAGCTCAGATGAGAG 96
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Qy      20 LeuSerIleThrThrProGlnIleMetIleGlnLysAlaLysGIyGlnThrAlaTyRLeu 39
Db      97 TTGACAGTCCCGCCGGGCTCAAAATGGAAGCGGTAGAGGAGAAAGAGTGTGCTC 156
Qy      40 ProCysArgPheThrLeuLysProGlnAsp-----GlnGIyProLeu 53
Db      157 CCGGCTGTGATCAGATGGACGAGAGTGTGTCTCCACCCCGGAGGTGCCATC 216
Qy      54 AspIleGIyTrpLeuLeuSerProAlaAspAsnGlnValAspGlnValIleIleLeu 73
Db      217 CTGATC---TGTTCTTGGA---CAGAAGGAGGAAGAACCAACAGGTGTGTCTTAC 270
Qy      74 TyRserGIyAspLysIleTyRAspAspTyRTrpGlnAspLeuLysGIyArg-----Val 91
Db      271 ATTAATGGA-----GTATGACAAATAAATCACTGGAACACCCCTGTGTC 312
Qy      92 HisPheThrSerAsnAspLeuLysSerGIyAspAlaSerIleAsnValThrAsnLeuGln 111
Db      313 CAC-----TCATCTCTTCACGAAATGTCTCTCGCGCGGCGCACTTCAG 360
Qy      112 LeuSerAspIleGIyThrTyRGIyCysLysValLys-----LysAla 125
Db      361 GAGGAGACTCTGGGACTTACCGCTTCTGTCAATGTGACAGATGATGAAGCAAAAT 420
Qy      126 ProGIyValGIyAsnLysLysIleGlnLeuThrValLeuLeuLysProSerGIyThrArg 145
Db      421 ATAGGCCACAGCATCAAAAGCATPAGAGCTCAAAAGTCTGTTCCCTCAGCTCCATCC 480
Qy      146 CysTyRValAspGIySerGIyGlnIleGlnLeuThrValLeuLeuLysCysGlnProLys 165
Db      481 TGTAGTTACAGGGGTGTACCTATGTGCGGACCAATGTACCTGAACATGCAAGTCCCA 540
Qy      166 GlnGIySerLeuProLeuLeuTyRGIyTrpGlnLysLeuSerAsnSerGlnLysLeu--- 184
Db      541 AGGAGTAAACCTACTGCTCTAGTACAGTGGAGAGGCTGCCCCATCTCCAGGCTTTC 600
Qy      185 -----ProThrLeuTrpLeuAlaGlnMetThrSerProValIleSerValLysAla 202
Db      601 TTGGACCAAGCTTA-----GATGCTGTTCGTGATCTTTAAAGCTACTACTACTT 651
Qy      203 SerThrGlnTyRserGIyThrTyRserCysThrValLysAsnArgValGIySerAspGln 222
Db      652 TCCATTGCCATGTCTGAGCTATGTCTGCAAGGCTCAAAACAGATGGGCTTTGGCAAG 711
Qy      223 CysLeuLeuArgLeuAspValValProProSerAsnArgAlaGIyThrIleAlaGIyAla 242
Db      712 TGCAAGTCACTTGGACGTGATGACAGGCTC---AAGCTGCACTGTGCTGGAGCA 768
Qy      243 ValIleGIyValLeuLeuAlaLeuValLeuIle---GlyLeuIleIle 257
Db      769 GTTGTGGCACTTTGTTGTGGTTGGTGTGATGAGTGGGCTGTGCTGT 816
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RESULT 14

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US-09-336-536-37
; Sequence 37, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336,536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 1846
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-336-536-37
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Alignment Scores:

Qy 3 LeuLeuLeuCysPheValLeuLeuCysGIyValAlaAspLeuThrArgSer----- 19
Db 37 CTGGGGGTTTGTCTCGGACCTGATGTAACCTTGTCTTCCGAGCTCAGATGAGAG 96

Pred. No.: 1.13e-20 Length: 1846
Score: 246.50 Matches: 79
Percent Similarity: 47.46% Conservative: 52
Best Local Similarity: 28.62% Mismatches: 108
Query March: 18.14% Indels: 37
DB: 4 Gaps: 12

US-09-899-634c-2 (1-261) x US-09-336-536-37 (1-1846)

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QY 3 LeuLeuLeuCySpheValLeuLeuCyGlyValAlaAspLeuThrArgSer----- 19
DB 143 CTGCGGGTTTGTCTCTGGAGTGAATACCTTCTGCTCCCTCCGAGTCAAGATGAG 202
QY 20 LeuSerIleThrThrProGluGlnMetIleGluValAlaValGlyGluThrAlaTyrl 39
DB 203 TTGCAAGTGGCCCCGGGCGCTCAACAATTTGAAGCCGTAGAGGAGAGAAAGATGTGCTC 262
QY 40 ProCyArgPheThrLeuGlyProGluAsp-----GlnGlyProLeu 53
DB 263 CCGGCTGTGACGATGGACGCGAGAGTGTGTCCACCCCGGAGGTGCTCATC 322
QY 54 AspIleGluTrpLeuLeuSerProAlaAspAsnGlnValAlaAspGlnValIleLeu 73
DB 323 CTGATC---TGTTCTTGGAA---CAAGAAAGGAGAGAACCAACAGGTTCTTCTT 376
QY 74 TySerGlyAspIleTyrlAspAspTyrlTyrlAspLeuGlyArg-----Val 91
DB 377 ATTAATGGA-----GTCATGACAAATTAACCTGGAACAGCCCTGTGTC 418
QY 92 HisPheThrSerAsnAspLeuGlySerGlyAspAlaSerIleAsnValThrAsnLeuGln 111
DB 419 CAC-----TCTATCTCTTACGGAATGTGCTCTGCGCGGCGGCACTCCAG 466
QY 112 LeuSerAspIleGlyThrTyrlGlnCySlyValLys-----LysAla 125
DB 467 GAGGAGACCTCTGGAGCTTACCCCTGTCTGTCAATGTGCAGATGATGAGGCAAAAGT 526
QY 126 ProGlyValGlyAsnLysIleGlnLeuThrValLeuLeuLysProSerGlyThrArg 145
DB 527 ATAGGCGACAGCATCAAAAGCATAGAGCTCAAAAGTGTGTCTCTCCAGTCTCCATCC 586
QY 146 CysTyrlValAspGlySerGluGluIleGlyAsnAspPheLysLeuLysCysGluProLys 165
DB 587 TGTAGTTTACAGGGGTACCTTATGTGCGGAGCAACATGTACCTGTAACCTGCAAGTCCCA 646
QY 166 GluGlySerLeuProLeuLeuTyrlGluTrpGlnLysLeuSerAsnSerGlnLysLeu 184
DB 647 AGGAGTAACCTACTGCTCACTACAGTGGAGAGGCTGGCCCCCATCTCCCAAGTCTTC 706
QY 185 -----ProThrLeuTrpLeuAlaGluMetThrSerProValIleSerValLysAsnAla 202
DB 707 TTGGAACAGCCCTTA-----GATGCTGTTCGTGATCTTTAAAGCTCACTAACTCT 757
QY 203 SerThrGluTyrlSerGlyThrTyrlTyrlSerCysThrValLysAsnArgValGlySerAspGln 222
DB 758 TCCATTGCTCATGTCTGAGTCTATGTCTGCAAGCGCTCAAAACAGAGGGGCTTTGGCAAG 817
QY 223 CysLeuLeuArgLeuAspValAlaProProSerAsnArgLacIleThrIleAlaGlyVal 242
DB 818 TGGACAGTACCTTGGACGTGATGACAGGGTCC---AAGGCTCACTGCTGCTGGAGCA 874
QY 243 ValIleGlyValLeuLeuAlaLeuValIleLeuGlyLeuIleLeu 257
DB 875 GTTGTGGGCACTTTTGTGTGGTGTGTCTGATAGCTGGGCTGTCTCTG 922
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RESULT 15
US-08-979-424-2
; Sequence 2, Application US/08979424
; Patent No. 5942606

; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN

NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastsEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,424
FILING DATE: Filed Herewith
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0405 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1387 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: LUNGEFT03

CLONE: 1232054

US-08-979-424-2

Alignment Scores:
Pred. No.: 3.34e-17 Length: 1387
Score: 217.00 Matches: 70
Percent Similarity: 41.99% Conservative: 48
Best Local Similarity: 24.91% Mismatches: 113
Query March: 15.97% Indels: 50
DB: 2 Gaps: 11

US-09-899-634c-2 (1-261) x US-08-979-424-2 (1-1387)

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QY 3 LeuLeuLeuCySpheValLeuLeuCyGlyValAlaAspLeuThrArgSer---LeuSer 21
DB 161 CTGCGGTTTGTCTCTGGGCTGAGTGCCCTCGGCCCCCTCGGGGCCAGCTGC 220
QY 22 IleThrThrProGluGlnMetIleGluValAlaValGlyGluThrAlaTyrlLeuProCys 41
DB 221 CTGCACTTCCCGCAACCGGCTTGCAGCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 280
QY 42 ArgPheThrLeuGlyProGlu-----AspGlnGlyProLeuAspIleGlu 56
DB 281 TGGTACACCTTGCACGCGGAGGTGTCTTCATCCCAAGCCATGGAGGTGCCCTTTGTGATG 340
QY 57 TrpLeuLeuSerProAlaAspAsnGlnLysValAspGlnValIleLeuTyrlSerGly 76
DB 341 TGGTCTTCAAA-----CAGAAAGAAAAGAGATCAGGTGTGTCTCACTCAATGGG 394
QY 77 -----AspIleTyrlAspAspTyrlTyrlGlnAspLeuLys 88
DB 395 GTCACACAAGCAAACTGTGATCTCTGCTAC----- 430
QY 89 GlyArgValHisPheThrSerAsnAspLeuGlySerGlyAspAlaSerIleAsnValThr 108
DB 431 -----TCCATGCCCTCCCGAAGCTGTCTCTGCGGCTGGAG 466
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QY 109 AsnLeuGlnLeuSerAsp11IeGlyThrTyGlnCysIysValIys----- 123
    |||||
    |||||
Db 467 GGTCTCCAGAGAAAGACTGCGCCCTACAGCTGCTCCGTAATGTGCAAGCAACAA 526
    |||||
QY 124 ---LysAlaProGlyValGlyAsnIysLysIleGlnLeuThrValIleLeuLysProSer 142
    |||||
    |||||
Db 527 GGCMAATCTAGGGCCACAGCATCAAAACCTTAGACTCAATGTACTGTCTCTCCAGCT 586
    |||||
QY 143 GlyThrArgCysTyValAspGlySerGluGluIleGlyAsnAspPheLysLeuLysCys 162
    |||||
    |||||
Db 587 CCTCATCTCGCGCTCTCCAGGGGTGTGCCCATGTGGGGGCAACGTGACCTGAGCTGC 646
    |||||
QY 163 GluProLysGluGlySerLeuProLeuLeuTyGluTrpGlnLysLeuSerAsnSerGln 182
    |||||
    |||||
Db 647 CAGTCTCAAGAGTAAGCCCGCTGTCCAATACCAAGTGGATCGG----- 691
    |||||
QY 183 LysLeuProThrLeuTrp-----LeuAlaGluMetThrSerProValIle 197
    |||||
    |||||
Db 692 CAGCTTCCATCTCTCCAGACTTCTTTGCACACAGCATTAAGATGTCAATCCGTGGGCTTTTA 751
    |||||
QY 198 SerValIysAsnAlaSerThrGluTrpSerGlyThrTySerCysThrValIysAsnArg 217
    |||||
    |||||
Db 752 AGCCTCACCAACCTTTGTGTCTTCATGAGTGTGAGTCTATGTCTGCAAGGCCCAATGAG 811
    |||||
QY 218 ValGlySerAspGlnCysLeuLeuArgLeuAspValIleProProSerAsnArgAlaGly 237
    |||||
    |||||
Db 812 GTGGGCACTGCCCAATGTAAATGTGACGCTGAA---GTGAGCACAGGGGCTGGAGCTGCA 868
    |||||
QY 238 ThrIleAlaGlyAlaValIleGlyValLeuLeuAlaLeu---ValLeuIleGlyLeuIle 256
    |||||
    |||||
Db 869 GTGGTGTCTGAGCTGTGTGGGTACCTGTGTGACTGGGGTGTGCTGGGCTGTGTC 928
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QY 257 Ile 257
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Db 929 CTC 931
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Search completed: July 12, 2003, 13:00:48
Job time : 53 secs

GenCore version 5.1.6
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OM proteoin - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 12:41:12 ; Search time 138 Seconds
(without alignments)
2986.361 Million cell updates/sec

Title: US-09-899-634C-2

Sequence: 1 MALLLCFVLICGVADITRSL.....AVIGVLLALVILGLIFCCR 261

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Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1105431 seqs, 789497651 residues

Total number of hits satisfying chosen parameters: 2210862

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications NA -QEXT=fastp -SURF1=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=plc -NORM=ext -HEADSIZE=500 -MINLEN=0
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Database : Published Applications NA:

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1359	100.0	4286	10	US-09-899-634A-1
2	1353	99.6	1098	10	US-09-899-634A-3
3	1238	91.1	2434	10	US-09-971-736-1
4	1238	91.1	2473	9	US-10-176-847-77

5	1238	91.1	3060	9	US-09-992-598-504	Sequence 504, App
6	1238	91.1	3060	9	US-09-989-293A-504	Sequence 504, App
7	1238	91.1	3060	9	US-09-989-735-504	Sequence 504, App
8	1238	91.1	3060	9	US-09-990-444-504	Sequence 504, App
9	1238	91.1	3060	9	US-10-053-107-9	Sequence 9, Appl
10	1238	91.1	3060	9	US-09-989-730-504	Sequence 504, App
11	1238	91.1	3060	9	US-09-990-438-504	Sequence 504, App
12	1238	91.1	3060	9	US-09-991-181-504	Sequence 504, App
13	1238	91.1	3060	9	US-09-993-687-504	Sequence 504, App
14	1238	91.1	3060	9	US-09-989-734-504	Sequence 504, App
15	1238	91.1	3060	9	US-09-997-653-504	Sequence 504, App
16	1238	91.1	3060	9	US-09-993-687-504	Sequence 504, App
17	1238	91.1	3060	9	US-09-990-438-504	Sequence 504, App
18	1238	91.1	3060	9	US-09-990-562-504	Sequence 504, App
19	1238	91.1	3060	9	US-09-997-428-504	Sequence 504, App
20	1238	91.1	3060	9	US-09-997-666-504	Sequence 504, App
21	1238	91.1	3060	9	US-10-227-884-215	Sequence 215, App
22	1238	91.1	3060	9	US-09-990-711-504	Sequence 504, App
23	1238	91.1	3060	9	US-10-230-163-215	Sequence 215, App
24	1238	91.1	3060	9	US-09-989-726-504	Sequence 504, App
25	1238	91.1	3060	9	US-09-990-437-504	Sequence 504, App
26	1238	91.1	3060	9	US-09-998-156-504	Sequence 504, App
27	1238	91.1	3060	9	US-10-218-631-215	Sequence 215, App
28	1238	91.1	3060	9	US-10-230-338-215	Sequence 215, App
29	1238	91.1	3060	9	US-09-991-157-504	Sequence 504, App
30	1238	91.1	3060	9	US-09-991-172-504	Sequence 504, App
31	1238	91.1	3060	9	US-09-991-514-504	Sequence 504, App
32	1238	91.1	3060	9	US-09-997-573-504	Sequence 504, App
33	1238	91.1	3060	9	US-10-230-414-215	Sequence 215, App
34	1238	91.1	3060	9	US-09-990-443-504	Sequence 504, App
35	1238	91.1	3060	9	US-09-997-559-504	Sequence 504, App
36	1238	91.1	3060	9	US-09-990-726-504	Sequence 504, App
37	1238	91.1	3060	9	US-09-997-601-504	Sequence 504, App
38	1238	91.1	3060	9	US-09-989-728A-504	Sequence 504, App
39	1238	91.1	3060	9	US-09-990-440-504	Sequence 504, App
40	1238	91.1	3060	9	US-09-991-854-504	Sequence 504, App
41	1238	91.1	3060	9	US-09-997-349-504	Sequence 504, App
42	1238	91.1	3060	9	US-09-997-440-504	Sequence 504, App
43	1238	91.1	3060	9	US-09-997-628-504	Sequence 504, App
44	1238	91.1	3060	9	US-09-997-688-504	Sequence 504, App
45	1238	91.1	3060	9	US-10-213-145-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-899-634A-1
; Sequence 1, Application US/0989634A
; Patent No. US20020059654/1
; GENERAL INFORMATION:
; APPLICANT: Thomas Buehler, Reto Andreas Gadiant, Reinhard Korn, Rao Movva
; TITLE OF INVENTION: PCR and its uses
; FILE REFERENCE: 4-31499A
; CURRENT APPLICATION NUMBER: US/09/899,634A
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: porcine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3229)..(4014)
US-09-899-634A-1

Alignment Scores:

Pred. No.:	8,61e-172	Length:	4286
Score:	1359.00	Matches:	261
Percent Similarity:	100.00%	Mismatch:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

GENERAL INFORMATION:									
APPLICANT:	No. US20020132769A1arctis AG								
TITLE OF INVENTION:	Targeting molecules								
FILE REFERENCE:	4-31615/GTI								
CURRENT APPLICATION NUMBER:	US/09/971,798								
CURRENT FILING DATE:	2001-10-05								
NUMBER OF SEQ. ID NOS:	31								
SOFTWARE:	PatentIn version 3.1								
SEQ ID NO 1									
LENGTH:	2434								
TYPE:	DNA								
ORGANISM:	Homo sapiens								
FEATURE:									
NAME/KEY:	CDS								
LOCATION:	(60)..(1157)								
OTHER INFORMATION:									
US-09-971-798-1									
Alignment Scores:									
Pred. No.:	6.8e-156	Length:	2434						
Score:	1238.00	Matches:	233						
Percent Similarity:	94.25%	Conservative:	13						
Best Local Similarity:	89.27%	Mismatches:	15						
Query Match:	91.10%	Indels:	0						
DB:	10	Gaps:	0						
US-09-899-634C-2 (1-261) x US-09-971-798-1 (1-2434)									
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DB	60	ATGGCGCTCTGCTGCTGCTTGTGCTCTGTGCGAGTGAAGTGGATTTCGCCAAGAGTTG	119						
QY	21	SerIleThrThrProGluInMetIleGluValAlaValSGIValGluThrAlaTyrLeuPro	40						
DB	120	AGTATCACTACTCTCTGAGAGATGATTGAAAAAGCAAGGGAACTGCTATCTCCG	179						
QY	41	CysArgPheThrLeuGluProGluAspGlnGlyProLeuAspIleGluThrLeuLeuSer	60						
DB	180	TGCAAATTTTCGCTTAGTCCCGAAGCAGGACCGCTGGACATCGAGTGGCTGATATCA	239						
QY	61	ProAlaAspAsnGlnValAspGlnValIleIleLeuTyrSerGlyAspValIleTyr	80						
DB	240	CCAGCTGATATATGAGAAAGGTGATCAAGTATTATTATTTTCGGAGACAAAATTTAT	299						
QY	81	AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer	100						
DB	300	GATGACTACTACTCAATCAATCTGAAAGGCCAGATGATTTTTCAGATGATGATCTCAATCT	355						
QY	101	GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys	120						
DB	360	GGTGATCATCATTAATGATGTAACGATTTTACAACTGTGAGATATGGCATATTCAGTGC	419						
QY	121	LysValIleLysValAlaProGluValGlyAsnLysValIleGlnLeuThrValLeuLeuLys	140						
DB	420	AAAGTGAATAAACCTCGGTGTTCGAAATTAAGAAATTCATCTGGTAGTCTTGTTAG	479						
QY	141	ProSerGlyThrArgCysTyrValAspGlySerGluGluIleGlyAsnAspPheLeuLeu	160						
DB	480	CTTTCAGGTCCGAGATTTTCGTTGATGATCTGAAAGATTTGGAAGTACCTTTAAGATA	539						
QY	161	LysCysGluProLysGluGlySerLeuProLeuLeuTyrGluThrGlnLysLeuSerAsn	180						
DB	540	AAATGTCAACCAAAAGAGGTTCACTTCATTTCAGATGAGTGGCAAAAATTTGTCTGAC	599						
QY	181	SerGlnLysLeuProThrLeuThrLeuAlaGluMetThrSerProValIleSerValLys	200						
DB	600	TCAAGAAATAATGCCACTTCATGTGTAGCAGAAATGACTTCATCTGTTATTCGTAAAA	658						
QY	201	AsnAlaSerThrGluTyrSerGlyThrTyrSerCysThrValLysAsnArgValGlySer	220						
DB	660	AAATGCTCTTCTAGTACTCTGGGAATATACAGCTGTACAGTGAAGAAAGAGTGGGCTCT	719						
QY	221	AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIleAla	240						

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Db      720 GATAGAGCGCTTGGCTGCTTAACGTTGCCCTCCTCCATTCAATAAAGCTGCATTAATTCGA 779
Oy      241 GtYAlaValIlegIyAlLeuLeuAlaLeuValleuilegIyleuilellepheCyS 260
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Db      780 GGAGCCATTATAGAACTTTGCTTGCTGTACGCGCATTTGGTCTTATCATCTTTGGCTG 839
Oy      261 Arg 261
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Db      840 CGT 842

RESULT 4
US-10-176-847-77
; Sequence 77, Application US/10176847
; Publication No. US20030068636A1
; GENERAL INFORMATION:
; APPLICANT: Velby, Pelter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/10/176, 847
; CURRENT FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 2473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-176-847-77

Alignment Scores:
Pred. No.:           6,97e-156             Length:         2473
Score:              1238.00                Matches:        233
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Best Local Similarity: 89.27%               Mismatches:    15
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Oy      21 SerLeThrThrPrpGluGlnMetIleGlnLysAlaLysGlyGlnThrAlaTyrlLeuPro 40
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Db      154 AGTATCACTACTCCTCGTAAGAAGATGATGAAAAGCCAAAGGGAAACTGCTATCTGCCA 213
Oy      41 CysArghPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluTrpLeuLeuSer 60
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Db      214 TGCAAAATTTCAGCTTACTCCCGAAGACCAGAGCACCGGTGACATCGATGATATCA 273
Oy      61 ProAlaAspaAngInLysValaAspGlnValIleIleLeuTySerGIyAspLysIleTy 80
          ||:::||
Db      274 CCAGCTGATATATCAAGAGGTGATCAAGATGATTATTATTATCTGGAGACAAATTAT 333
Oy      81 AspaSpLyrrTyrgInAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
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Db      334 GATACACTCAATCCAGATCTGAAAGCGCGATCAATTTVACGATATGATCTCAAAATCT 393
Oy      101 GlYAspaLaserIleasnValThrAsnLeuGlnLeuSerAspIleGIyThrrTyrgInCys 120
          |||||
Db      394 GGTATGCAATCAATMAATGTACGAAATTTCAACATGTCACATATTTGGCACATATCAGTGC 453
Oy      121 LysValLysLysAlaProGIyValaGlyAsnLysLysIleGlnLeuThrValLeuLeuLys 140
          |||||
Db      454 AAAGTGA AAAAGCTCCTGGTGTTCGCAAATTAAGAAGATTCATCTCGTGAATTCCTTTGAAG 513
Oy      141 ProSerGIyThrArgCysTyrrValaAspGlySerGIyGlnIleGlyLeuAsnAspPheLysLeu 160
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Db      514 CCTTCAGGTGCGAGATGTATCGTTGATGATCTGGAAGAAATTTGGAAGTGACTTTAAGATA 573

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QY 161 LysCysGluProLysGluGlySerLeuProLeuLeuTyrGluTyrGlnLysLeuSerAsn 180
Db 574 AATGTGAACCAAGAGAGGTCACTTCATTAAGATAGTGGCAAAATTTGTCTGAC 633
QY 181 SerGluLysLeuProTyrLeuTyrPleuAlaGluMetThrSerProValIleSerValys 200
Db 634 TCACAGAAATAGCCCATCTTATGCTTAGCAGAAATGACTTCATCTGTATATCTGTAA 693
QY 201 AsnAlaSerThrGluTyrSerGlyThrTyrSerCysThrValLysAsnArgValGlySer 220
Db 694 AATGCCCTTCTGATGCTCTGAGACATACAGCTGATCACTCAGAAACAGAGTGGCTCT 753
QY 221 AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIleAla 240
Db 754 GATCAGAGCTGTGTGCTTAACGTGTCTCCCTTCAATTAAGCTGAGCTAATTTGCA 813
QY 241 GAlaValIleGlyValIleLeuLeuAlaLeuValIleGlyLeuIleIlePecCysCys 260
Db 814 GGAGCATTATAGAGAACTTGTCTGCTAGCCGCTCATTTGTTATCATCTTTGCTGT 873
QY 261 Arg 261
Db 874 CGT 876

RESULT 5
US-09-592-598-504
Sequence 504, Application us/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
PRIORITY FILING DATE: 2001-11-14
PRIORITY APPLICATION NUMBER: 60/049787
PRIORITY FILING DATE: 1997-06-16
PRIORITY APPLICATION NUMBER: 60/062250
PRIORITY FILING DATE: 1997-10-17
PRIORITY APPLICATION NUMBER: 60/065186
PRIORITY FILING DATE: 1997-11-12
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PRIORITY FILING DATE: 1997-11-24
PRIORITY APPLICATION NUMBER: 60/075945
PRIORITY FILING DATE: 1998-02-25
PRIORITY APPLICATION NUMBER: 60/078910
PRIORITY FILING DATE: 1998-03-20
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PRIORITY FILING DATE: 1998-04-28
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APPLICANT: Baker, Kevin P.
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
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CURRENT FILING DATE: 2001-11-20
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Score: 1238.00 Matches: 233
Percent Similarity: 94.25% Conservative: 13
Best Local Similarity: 89.27% Mismatches: 15
Query Match: 91.10% Indels: 0
DB: 9 Gaps: 0

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US-09-899-634c-2 (1-261) x US-09-899-293A-504 (1-3060)

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QY 21 Ser1eThrThrProGluGlnMetIleGluValAlaGlyGluThrAlaTyrLeuPro 40

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DB 257 CCAGCTGATTAATCAAGAGGTGATCAAGATTAATTAATTCGAGACAAATTTAT 316
QY 81 AspAspIlyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAspLeuLysSer 100
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QY 101 GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys 120
DB 377 GGTGATGATCATTAATGATTAAGATTAATTTACACTGTCAGATATGGCATATCATGTC 436
QY 121 LysValLysLysAlaProGlyValGlyAsnLysIleGlnLeuThrValLeuLys 140
DB 437 AAGTGAAGAAAGCTCTGCTGCTTGCATAAAGAAGATTCATCTGAGTCTTGTAG 496
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DB 737 GATCAGTCTCTTTCGCTTAACGTTGCTCTCTTCAATTAAGCTGGAATTAATTGCA 796
QY 241 GlyAlaValIleGlyValLeuLeuAlaLeuValLeuIleGlyLeuIleIlePheCysCys 260
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QY 261 Arg 261
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RESULT 7

US-09-989-735-504
Sequence 504, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavira, Iyer J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

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APPLICANT:	Roy, Margaret Ann
APPLICANT:	Stewart, Timothy A.
APPLICANT:	Tunas, Daniel
APPLICANT:	Watanabe, Colin K.
APPLICANT:	Williams, P. Mickey
APPLICANT:	Wood, William I.
APPLICANT:	Zhang, Zemin
TITLE OF INVENTION:	Secreted and Transmembrane
TITLE OF INVENTION:	Acids Encoding the Same
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PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089618
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089655
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089801
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PRIOR FILING DATE:	1998-06-22
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PRIOR APPLICATION NUMBER:	60/090429
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PRIOR APPLICATION NUMBER:	60/090540
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090542
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090557
PRIOR FILING DATE:	1998-06-24

[illegible]

PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
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PRIOR FILING DATE: 1998-06-23
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PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	9,76e-156	Length:	3060
Score:	1238.00	Matches:	233
Percent Similarity:	94.25%	Conservative:	13
Best Local Similarity:	89.27%	Mismatches:	15
Query Match:	91.10%	Indels:	0
DB:	9	Gaps:	0

US-09-899-634c-2 (1-261) x US-09-899-730-504 (1-3060)

QY 1 MetAlaLeuLeuLeuCySphValLeuLeuCyGlyValAlaAspLeuThrArgSerLeu 20
|||||
DB 77 ATGGCGCTCTCTGCTTCGTCCTCGCGGAGTGTGATTCGCCAGAACTTG 136
|||||
QY 21 SerIleThrThrProGluMetIleGluValAlaValGlyGluThrAlaTyrLeuPro 40
|||||
DB 137 AGTATCACTACTCTCGAAGATGATTGAAAAGCCAAAGGGGAACTCCCTATCTGCCA 196
|||||
QY 41 CysArgPheThrLeuGlyProGluAspGinglyProLeuAspIleGluTrpLeuSer 60

Db 197 TCGAATTTACGCTTACTCCGAGACAGGACCGCTGACATCGAGTGGCTGATATCA 256
Qy 61 ProAlaAspAsnGlnValAspGlnValIleIleLeuTyrSerGlyAspLysIleTyr 80
Db 257 CCAAGCTATATACGAAGGTGATCAAGTATTTATTTATTTCTGAGACAAAATTTAT 316
Qy 81 AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuSer 100
Db 317 GATGACTACTATCCAGATCTGAAGGCGAGTCAATTTTCAGATATGATCTCAAACT 316
Qy 101 GLYAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys 120
Db 377 GGTGATGTCATCAATTAATGTACCAATTCAACTGCAATATTTGGCAATATCACTGC 436
Qy 121 LysValLysLysAlaProGlyValGlyAsnLysLysIleGlnLeuThrValLleuLys 140
Db 437 AAAGTGAANAAGCTCTGCTGTTGCANAATGAGAAATTCATCTGTAAGTTCTTTAG 496
Qy 141 ProSerGlyThrArgCysTyrValAspGlySerGlnGlnIleGlyAsnAspPheLysLeu 160
Db 497 CTTTCAGGTGAGATGTTACGTTGATGATCTGAAGAAATTTGGAAGTGAAGTCAATTA 556
Qy 161 LysCysGlnProLysGlnGlySerLeuProLeuLeuTyrGlnTyrGlnLysSerAsn 180
Db 557 AAATGTGACCAAAAGAGGTTCACTTCATTCAGATATGAGTGGCAAAAATTTGCTGAC 616
Qy 181 SerGlnLysLeuProThrLeuTyrPheLysGlnLeuThrSerProValIleSerValLys 200
Db 617 TCACGAAATATGCCCATCTTATGTTGCGAAGAAATGCTTCATCTGTAATCTGTAAGA 676
Qy 201 AsnAlaSerThrGlnTyrSerGlyThrTyrSerCysThrValLysAsnArgValGlySer 220
Db 677 AATGCTCTTCTGAGTACTCTGGGACATACAGCTGATCAGACGAAACAGAGTGGCTCT 726
Qy 221 AspGlnCysLeuLeuAspValValProProSerIleAsnArgAlaGlyThrIleAla 240
Db 737 GATCAGAGCTGTTGCTGCTAAACGTTGCTCCCTTCAATTAAGCTGCAATTAATGCA 796
Qy 241 GLYAlaValIleGlyValLleuLeuAlaLeuValLleuIleGlyLeuIleIlePheCysCys 260
Db 797 GAGGCCATTATAGGAACCTTGCTTCTGCTAGCCGCTCATTTGCTTATCATCTTTGCTGT 856
Qy 261 Arg 261
Db 857 CGT 859

RESULT 11
US-09-990-436-504
Sequence 504, Application US/09990436
Publication No. US20020198148A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K.

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
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PRIOR FILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/087759
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PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826

QY 161 LysCysGlnProlysglySerleuProleuLeuTyrglutrpGlnlySleuSerAsn 180
Db 557 AAATGTAAACCAAAAGAAAGTTCACTTCCATTACAGATGAGTGGCAAAAATGTCTGAC 616
QY 181 SerGlnlySerProtrleuTrleuTrleuAlaGlnWerTherSerProValIleSerValys 200
Db 617 TCAAGAAAATGCCACTTCAATGATTAGCAAAAATGACTTCACTGTTATATCTGTAATA 676
QY 201 AsnAlaSerThrglyTryserglyThrTyserCysThrValylsAsnArgValGlySer 220
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QY 221 AspGlnCysleuLeuAlaGlyLeuAspValValProProSerAsnArgAlaGlyThrIleAla 240
Db 737 GATCAGAGCCTGTGTGCTCTAAACGTTGCTCTTCAAAATAAAGCTGAGCTAATTGCA 796
QY 241 G1yAlaValIleGlyValIleleuAlaIleValleuIleGlyleuIleIlepeCysCys 260
Db 797 GGAAGCAATTAAGAACTTGTGCTGTAGCGCTCATGAGCTTATCATCTTTGTGT 856
QY 261 Arg 261
Db 857 CGT 859
RESULT 12
US-09-991-181-504
; Sequence 504, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyere, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaudi, J. Christopher
; APPLICANT: Guirney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
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; PRIOR APPLICATION NUMBER: 60/083322

; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17

	:	PRIOR FILING DATE: 1998-07-02	:
	:	PRIOR APPLICATION NUMBER: 60/091978	:
	:	PRIOR FILING DATE: 1998-07-07	:
	:	PRIOR APPLICATION NUMBER: 60/091982	:
	:	PRIOR FILING DATE: 1998-07-07	:
	:	PRIOR APPLICATION NUMBER: 60/092182	:
	:	PRIOR FILING DATE: 1998-07-09	:
Alignment Scores:			
Pred. No.: 9,76e-156 Length: 3060			
Score: 1238.00 Matches: 233			
Percent Similarity: 94.25% Conservative: 13			
Best Local Similarity: 89.27% Mismatches: 15			
Query Match: 91.10% Indels: 0			
DB: 9 Gaps: 0			
US-09-899-634C-2 (1-261) x US-09-991-181-504 (1-3060)			
OY	1	MetAlaleuleuleuCysPheValIleuleuCysGlyValAlaAspleuthrArgSerLeu	20
Dd	77	ATGGCCCTCGTGTGGCTTCGTGCTCGTGCGAGTAGTGATTGCCAGAAGTTTG	136
OY	21	SerLleThrThrProGlInMetIleGluysAlatysGlyUTRAtaTyLeuPro	40
Dd	137	AGTACACTACTCTGAAGAGATGTGAAGAAAGCCAAGGGAGAACTGCCTATCTCCA	196
OY	41	CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspiIleGluTrpLeuSer	60
Dd	197	TGGCAATTATACGCTTAGTCCGAGAACAGGACCCTCGACATCGAGTGGCTGATATCA	256
OY	61	ProAlaAspAsnGlnLysValAspGlnValIleileutyrsGrgLyAspLysIleTyr	80
Dd	257	CCAGCTCATATATAGAAGGTGATCAAGTATATTATTTATTCCTGGAGCAAATTTAT	316
OY	81	AspAspTyTYrGlnAspleuleuglyArgValHisPheThrserAsnAspleuleySer	100
Dd	317	GATGACTACTATCTCAATATCTGAAGCCGAGATCTTTAGAGTAATGATCTCAATCT	376
OY	101	GlyAspAlaserIleasnValThrAsnleuGlnleuSerAspiIleGlyThrTyGlnCys	120
Dd	377	GGTGAATCATCAATAATTAATTAACGAATTTACAACGTGATATTTGGCACATATCACTGC	436
OY	121	LysValLysLysAlaProGlyValGlyAsnLysIleGlnleuthrValIleuleuLys	140
Dd	437	AAAGTGA AAAAGCTCTCGTGTGCAATAAGAAATTCACTGTGATGTTCTTGTAAG	496
OY	141	ProSerGlyThrArgCysTyrtValasnglySerGluGluIleGlyAsnAspPheLysLeu	160
Dd	497	CCTTCAGGTGCGGAGTATGACCTTATGATGATCTGMAAGAAATGGAGACTTTTAAATA	556
OY	161	LysCysGluProArgGlnGlySerLeuProleuLeuTyRGluTrpGlnLysLeuSerAsn	180
Dd	557	AAATGTGAACCAAAAAGAGGTTCACTTCATTACAGTATGAGTGGCAAAAAATTTGTCGAC	616
OY	181	SerGlnLysLeuProThrLeuTrpLeuAlaGluMetThrSerProValIleSerValLys	200
Dd	617	TTCAGAAAATGCCCACTTCATGGTTAGAGAAAATGACTTCATGTTATATCTGTA AA	676
OY	201	AsnAlaserThrigLutryrsGrgLyThrTyrsCysThrValLysAsnArgValGlySer	220
Dd	677	AATGCCCTCTTCTGATGACTCTGGGACATACAGCTGTACAGCAAGACAGGTGGCTCT	736
OY	221	AspGlnCysleuleumArgleuaspyValProProserAsnAspGlaGlyThrIleAla	240
Dd	737	GATCAGGCTGTGTGGCTTAAACGTGTGCTCTTAAATTAAGCTGACCTAATTGCA	796
OY	241	GlyAlaValIleGlyValIleuleuAlaValleuIleGlyLysleuIleIlePheCysCys	260
Dd	797	GGAGCCATTATAGAACTTTGCTTCTCTAGGCGCTCATTTGCTTATCATCTTTTGGCTG	856
OY	261	Arg 261	
Dd	857	CGT 859	

RESULT 13
US-09-993-687-504
Sequence 504, Application US/09993687
Publication No. US20020198149A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C11
CURRENT APPLICATION NUMBER: US/09/993.687
CURRENT FILING DATE: 2002-11-14
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Oy      61  ProIlaAspAsnGlnIleValAspGlnValIleIleLeuTyrSerGlyAspIleTyr 80
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; Publication No. US20030003531A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, V. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC64
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[illegible]

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 11:49:47 ; Search time 1102 Seconds

(without alignments)
3835.773 Million cell updates/sec

Title: US-09-899-634C-2

Perfect score: 1359

Sequence: 1 MALLCPRLVLCVADLTRSL.....AVIGVLAVLIGLIIIFCCR 261

Scoring table:

BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1197	88.1	1022	13	BM547121
4	1136.5	83.6	864	13	BM64437
5	1129.5	83.1	922	13	BM754365
6	1105	81.3	879	9	AU131437
7	1084	79.8	956	13	BM649353
8	1060	78.0	824	9	AL534436
9	1049	77.2	775	13	BM67131
10	1019	75.0	779	13	BM080376
11	1015	74.7	885	9	AL555497
12	1004	73.9	680	13	BM537136
13	935	68.8	885	13	BM83597
14	913.5	67.2	702	13	BM77977
15	909.5	66.9	838	9	AL514786
16	890	65.5	677	10	BB65941
17	864.5	63.6	753	10	BE545085
18	855.5	63.0	915	14	BO895050
19	855	62.9	727	12	BM718557
20	843	62.0	644	10	BB66153
21	824	60.6	831	9	AL709335
22	818	60.2	928	12	BF583890
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24	748	55.0	970	12	BF164005
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32	608.5	44.1	667	10	BE292163
33	599	44.0	331	14	W33780
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REFERENCE 1 (bases 1 to 917)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polyes, D.
TITLE Full-length cDNA libraries and normalization


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/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT      223 a      225 c      222 g      194 t
ORIGIN

Alignment Scores:
Pred. No.:      1,2e-118      Length:      864
Score:          1136.50      Matches:      221
Percent Similarity: 90.04%      Conservative: 14
Best Local Similarity: 84.67%      Mismatches: 24
Query Match:      83.63%      Indels:      2
DB:              13          Gaps:          1

US-09-899-634C-2 (1-261) x B1684437 (1-864)

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 922)
AUTHORS
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.jnl.gov
Place: LHAM1484 row: c column: 05
High quality sequence stop: 745.
Location/Qualifiers
1. 922
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5197372"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 019. Note:
this is a NIH MGC Library."
BASE COUNT      274 a      199 c      207 g      242 t
ORIGIN

Alignment Scores:
Pred. No.:      8.38e-118      Length:      922
Score:          1129.50      Matches:      221
Percent Similarity: 90.49%      Conservative: 17
Best Local Similarity: 84.03%      Mismatches: 21
Query Match:      83.11%      Indels:      4
DB:              13          Gaps:          1

US-09-899-634C-2 (1-261) x B1754365 (1-922)

QY      2 AlaleuLeuLeuCySpheValleuLeuCyGlyValAlaAspLeuThrArgSerLeu 21
      |||||
Db      2 GCGCTCCTGCTGCTTCCGTCCTGTCGGGAGTATTCGCGCAAGATTGAGT 61
QY      22 IleThrThrProGluGlnMetIleGluValAlaGlyGluThrAlaTYrLeuProCys 41
      |||||
Db      62 ATCACTACTCTCGAAGATGATTAAGAAAGCCAAAGGGGAAACTGCTATCTGCAATGC 121

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QY	42	ArgherhtrleuglyProGlaAspGlaGlyProLeuAspIleGlyTrpLeuLeuSerPro	61
Db	122	AAATTTCAGCTTACTGCCGAAGACCGAGACCGCTGCACATCGAGTGCCTATATCACCA	181
QY	62	AlaAspAsnglnIysValAspGlnValIleIleLeuTySerGlyAspIysIleTyAsp	81
Db	182	GCTGATATATCAAGAAAGGTGATCAAGTATTTATTTATCTCGGAGCAAAATTTATGAT	241
QY	82	AspTyTrpGlnAspLeuLeuGlyValArgValHisPheThrSerAsnAspLeuLeuSerGly	101
Db	242	GACTACTATCCAGATCTCGAAAGGCCGAGTACATTTTACAGATTAATGATCTCAATCTGGT	301
QY	102	AspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyGlnCysIys	121
Db	302	GATCATCATAAATTAATATGTAACAAATTTACAACTGTCAGATATTGGACATATCAGTGCAA	361
QY	122	ValIysIysValAspProGlyValAlGlyAsnIysIysIleGlnLeuThrValLeuLeuLeuSerPro	141
Db	362	GTGAAAAAAGCTCTCGTGTTGCCAATTAAGAAGATTCATCTGGTATGTTCTTGTTAAGCT	421
QY	142	SerGlyThrArgCysTyTrpValAspGlySerGluGluIleGlyAsnAspPheIysLeuIys	161
Db	422	TCAGGTGCGAATGTTACGTGATGAGCATCTGACAAATTTGAAAGTACATTTAAGATTAATA	481
QY	162	CysGluProIysGluGlySerLeuProLeuLeuTyTrpGlnIysLeuSerAsnSer	181
Db	482	TGTGATCCAAAGAAAGGTTCACCTTCATTAACATGATGAGGCAAAATTTGTCGTACCTCA	541
QY	182	GlnIysLeuProThrLeuTrpLeuAlaGluMetThrSerProValIleSerValIysAsn	201
Db	542	CAGAAAAAGCCCATCTTCATGGTTTGACAAATTAAGATTCATCTGTTATATCTGTAATAAAT	601
QY	202	AlaSerThrGluTyTrpSerGlyThrTySerCysThrValIys-AsnArgValIglySerAs	221
Db	602	GCTCTTCTGTAGTACTCTCGGACATACAGCTGATACAGTCAAGAAAAACAAGAGGCGCTCGA	661
QY	221	ProIleCysLeuLeuArgLeuAspValValProProSerSerAsnArgAlaGlyThr--IleAla	240
Db	662	TCAGGCTGTGTCCTCTTAACAGTGTGCTCCCTCTTCAATTAAGCTGACCTTACTTGCA	721
QY	241	GlyAlaValIle---GlyValLeuLeuAlaLeuValLeuIleGlyLeuIleIlePheCys	259
Db	722	GGAGCGCATTAATAGCAACACTTGTGCTTGTCTTAGCGCTCAATCGCTCTTATACATCTC	781
QY	260	Cys 260	
Db	782	TGC 784	
RESULT 6			
LOCUS	AU131437	879 bp	mRNA linear
DEFINITION	AU131437 NT2RP3 Homo sapiens cDNA clone NT2RP302577 5', mRNA		
ACCESSION	AU131437		
VERSION	AU131437.1		
KEYWORDS	EST.		
ORGANISM	human.		
SOURCE	Homo sapiens		
COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eubateria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 879) Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saiko,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T. HRI human cDNA project unpublished (2000) Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@nrl.co.jp		

FEATURES	source
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.	Location/Qualifiers 1..879

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RP3002577"
/clone_11b="NT2RP3"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/note="Vector: DME18SPu3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT      247 a      182 c      213 g      230 t      7 others
ORIGIN

```

Alignment Scores:	
Pred. No.:	4,76e-115
Score:	1105.00
Percent Similarity:	90.12%
Best Local Similarity:	84.19%
Query Match:	81.31%
DB:	9
Length:	879
Matches:	21
Conservative:	15
Mismatches:	24
Indels:	1
Gaps:	0

US-09-899-634C-2 (1-261) x AU131437 (1-879)

QY MetAlaLeuLeuLeuCysPheValIleuLeuCysGlyValAlaAspLeuThrArgSerLeu 20
Db ATGGCGCTCCTGTGTCGTTCTTGCTGCTCCTGTGCAGATGATGGGTTTCCGCAAAATTGG 147
QY SerIleThrThProGluGlnMetIleGluPsaIalysGlyGluThrAlaTyLeuPro 40
Db AGTATCACACTACTCTTGAAGAAGATGATTGAAAAAGCCAAGGGAAAACGTCTATCTGCCA 207
QY CyeArgPheThrIleuGlyProGluAspGlnGlyProLeuAspIleGluTPLeuLeuSer 60
Db TGGAAATTTAACGGTTTAGTCCCAACAACAGGACCGCTGCACATCGAGTGGCATATVCA 267
QY ProAlAspaSngInLysValAspGlnValIleIleLeuTyrsSerGlyAspLysIleTyR 80
Db CCAGCTGCATATACGAAGGTGCATGAAGATATTATTATTTCTGAGACAAATAATTAT 327
QY AspAspTyrtYrGlnAspLeuLysGlyArGValHispherThrSerAsnAspLeuLysSer 100
Db GATGACTACTACTCAGATCTGAAGAGCCGAGTACATTTTACGAGTAATGATCTCAAACTCT 387
QY GlyAspAlaserIleasnValThrTrsnLeuGlnLeuSerAspIleGlyThrTyGlnCys 120
Db GGGAATGACATCAATAATGATTAACGAATTTAACACTGCAATATTGGACATATCACTGTC 447
QY LysValLysLysAlaProGlyValGlyAsnuLysIleGlnLeuThrValLeuLeuLys 140
Db AAAGTGA AAAAGCTCTCTGCTGTTCGCAATTAAGAAGATTCACTGTAAGTCTCTTGTAAG 507
QY ProSerGlyThrArgCysTyrsValAspGlySerGluGlnIleGlyAsnAspPheLysLeu 160
Db CCTTCAGGTCCGAGATGTAAGTATGATGATCTGAAGAAATTTGGAAGTCACTTTTAACATA 567
QY LysCysGlnProLysGlnGlySerLeuProLeuLeuTyrgluTPGlnLysLeuSerAsn 180
Db AATATGTGAACCAAAGANGGTTCACCTTCATTACGTAAGTGAAGTGC AAAAATTTGTCGAC 627
QY SerGlnLysLeuProThrLeuTPLeuAlaGlnMetThrSerProValIleSerValLys 200
Db TCACAGAAAATGCCCACTTCATGTTAGAGAAAATGACTTCATCTGNATATATCGNAAAA 687
QY AsnAlaserThrigluTyrsSerGlyThrTyrsCysThrValLysAsnArgValGlySer 220
Db AATGCCCTCTGTAGTACTCTGGGACATACACTGTACAGTCAGAAAACAGATGGGCTCT 747
QY AspGlnCysLeuLeuArgLeuAspValPro-ProSerAsnArgAlaGlyThrIleAla 240

Db 748 GATCAATGCTGCTGCTTAAACGTTGCTCCCTTCTCAATTAAGCTGACTAATTC 807

QY 240 AGTAAValleleValleuValleu 252
 Db 808 AAGGAGCCATTTAGAACCTTGTGCTTCTTTA 844

RESULT 7
 LOCUS B1649353 956 bp mRNA linear EST 12-SEP-2001
 DEFINITION 603278089F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5318302 5',
 mRNA sequence.
 B1649353
 ACCESSION B1649353
 VERSION B1649353.1 GI:15563589
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Scturognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 956)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LIML at:
 http://image.liml.gov
 Plate: LIML1807 row: a column: 23
 High quality sequence stop: 797.
 Location/Qualifiers
 1. 956
 /organism="Mus musculus"
 /strain="129,C57BL/6J,FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5318302"
 /clone_lib="NCI CGAP Mam3"
 /tissue_type="tumor_gross tissue"
 /dev_stage="10 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
 library constructed by life technologies. Investigators
 providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
 Reference for transgenic model: Xu et al., Nature Genetics
 22, 37-43 (1999)."

BASE COUNT 253 a 242 c 251 g 210 t

ORIGIN

Alignment Scores:
 Pred. No.: 1.34e-112 Length: 956
 Score: 1084.00 Matches: 226
 Percent Similarity: 89.96% Conservative: 16
 Best Local Similarity: 84.01% Mismatches: 18
 Query Match: 79.76% Indels: 9
 DB: 13 Gaps: 0

US-09-899-634c-2 (1-261) x B1649353 (1-956)

QY 61 ProAlaaspanglnysValaaspinValleleleleuTyserGlyasplyleTy 80
 Db 277 CCCTGATPAPACAGATAGATGATCAAGTATCATTTGATCTCGAGCAAAATTTAT 336
 QY 81 AspaPTyTyrGlnlepleuTyserGlyArgValHisPheThrserAsnpleuTyser 100
 Db 337 GATTAATCTATCTCCGATCTGAAAGACCGGATCATTTTACGATACGATGCAAGTCT 396
 QY 101 GLYAsAlaserlleasenvAlThrAsnleuGlnleuSerAsp1leGlyThrTyrgInCys 120
 Db 397 GCGGACCATCTTAATATGATGACCAACTGCACTGCGACATGACACTTACCCAGTGC 456
 QY 121 lvsVallyslsValaProGlyValGlyAsnlyslsleGlnleuThrValleuLeuLys 140
 Db 457 AAGTAGAAGAACCCCTGGGCGTTGCAATTAAGAAATTCCTGACCCGTTCTGTTAAG 516
 QY 141 ProserGlyThrArgCysTyrgValaAspGlyserGlnleuGlyAsnAspPheLysLeu 160
 Db 517 CCTTCAGGTACAAGATGCTTCGATGATGATCGAAGACATGGAATGACTTCAAGCTTA 576
 QY 161 lvsCysGluProlyslGlyserleuProleu-LeuTyrgluTrpGlnLysleuSerAs 180
 Db 577 AATGTGAACCCAGAGAGGCTCCCTTCCACTACACTGTTGAATGGCAGAACTGTGCA 636
 QY 180 nserGlnLysleuProThrleuTrpLeuAlaGlnMetThrserProVal11eserVally 200
 Db 637 CTCACAGACAAATCCATACCCGATGCTGCGAGAAAGACGTCAACGTTATATCTGTGA 696
 QY 200 Asana1aserThrGlu-TyrserGlyThrTyserCysThrVallyAsnArgValGlyS 220
 Db 697 GAACGCCAGTCTGAGTAATTCGAGACATACAGCTGACAGGTTCAAAACAGAGTGCGCT 756
 QY 220 erAsp-GlnCysleuLeuArgleuAsp-ValValProProserAsnArgAla-GlyThr- 238
 Db 757 CTGACCCAGTATGCTGCGACTAGAACGTGTGCCACCTCAAAACGACCCGGAACGA 816
 QY 239 l1eAlaGlyAlaValleleVal--leuLeuAlaValleuile-Glyleu1lele 257
 Db 817 ATGCGCGGCGCGCTCATAGGAAGGCTTGCTGCTCATCGGGGCGCATCTTC 876
 QY 258 PheCysCys 260
 Db 877 TTCTGCTGT 885

RESULT 8
 LOCUS AL534436 824 bp mRNA linear EST 13-FEB-2001
 DEFINITION AL534436 LIT_FLO13_FBRn1 Homo sapiens cDNA clone CS0DF004YB08 5
 prime, mRNA sequence.
 ACCESSION AL534436
 VERSION AL534436
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 824)
 AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr.
 Location/Qualifiers
 1. 824
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DF004YB08"
 /clone_lib="LIT_FLO13_FBRn1"
 /dev_stage="pooled tissue from post conception fetuses (20
 week, 24 week and 26 week)"

/lab host="DH10B"
 /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
 cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-stranded cDNA was digested with Not I
 and cloned into the Not I and Eco RV sites of the
 pCMVSPORT 6 vector. Library was constructed by Life
 Technologies. Contact : Feng Liang Life Technologies, a
 division of Invitrogen 9800 Medical Center Drive Rockville
 Maryland 20850. USA Fax : (1) 301 610 8371 Email :
 fliang@life.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 257 a 163 c 149 g 236 t 19 others

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
5.66e-110	1060.00	93.39%	88.11%	78.00%	824	200	12	15	0	0

US-09-899-634C-2 (1-261) x AL534436 (1-824)

Qy	32	AlaTysGtGtGtTrrAlaTrrLeuProCysArpTherLeuGlyProGluAspGlnGly	51
Db	1	GCCTAAGGGAAGTCTGCTATCTGCTGCAATTTAGCTTACCCGGAAGACAGGGA	60
Qy	52	ProLeuAspTleGtTrrLeuLeuSerProAlaAspAngTlnYValAspGlnVal	71
Db	61	CCGCTGACATCGAGTGGCTGATATCACACCTGATATACGAAGGTGGATCAAGTGA	120
Qy	72	TleLeuTrrSerGtYAspTleValTrrAspAspTrrTrrGlnAspLeuValYrVal	91
Db	121	ATTATATCTTGAGACAAATTTATATATATATATATATATATATATATATATATAT	180
Qy	92	HisPheTrrSerAspLeuLeuSerGtYAspAlaSerTleAsnValThrAsnLeuGln	111
Db	181	CATTTCAGAT	240
Qy	112	LeuSerAspTleGtYThrTrrGlnCysAlaValYValYValYValYValYValYVal	131
Db	241	CTGTCAGATATATGACATATATATATATATATATATATATATATATATATATAT	300
Qy	132	LysTleGlnLeuTrrValLeuLeuLeuProSerGtYThrArGtYValYValYValY	151
Db	301	AAGATTCATCTGTAAGTCTGTAAGTCTGTAAGTCTGTAAGTCTGTAAGTCTGTA	360
Qy	152	GluGlnTleGtYAsnAspPheYsLeuYsCysGluProYsGluYsLeuProLeu	171
Db	361	GAGGAATTTGAGAGCTTTAAGATATATATATATATATATATATATATATATAT	420
Qy	172	LeuTrrGtTrrGtYLeuLeuSerAsnSerGtYLeuProTrrLeuTrrLeuTrrLeu	191
Db	421	CAGATATGAGTGGCAAAATTTGCTGACCTACAGAAATGCCACATTCATGTTGCA	480
Qy	192	MetTrrSerProValTleSerValYsAsnAlaSerTrrGtYTrSerGtYThrTrr	211
Db	481	ATGATTCATCTGTAATCTGTAATCTGTAATCTGTAATCTGTAATCTGTAATCTG	540
Qy	212	CysTrrValYsAsnArGtYValYsArGtYValYsArGtYValYsArGtYValYsAr	231
Db	541	TGTACAGTCAGAACAGAGTGGCTCTATATATATATATATATATATATATATAT	600
Qy	232	ProSerAsnArGtYValYsArGtYValYsArGtYValYsArGtYValYsArGtY	251
Db	601	CCTCAATTAAGTGGAGCTATATGACAGAGCATTATAGAACTTCTTCTCTACG	660
Qy	252	LeuTleGtYLeuTleLeuPhe	258
Db	661	CTCATTTGCTTATATCTTT	681

RESULT 9

B1687131
 LOCUS B1687131 775 bp mRNA linear EST 18-SEP-2001
 DEFINITION 603314974F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5354827 5',
 mRNA sequence.
 ACCESSION B1687131.1 GI:15649759
 VERSION B1687131.1
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 775)
 NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1M11902 row: c column: 20
 High quality sequence stop: 775.
 Location/Qualifiers

FEATURES

source

1. 775
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5354827"
 /clone_1ib="NCI CGAP Mam6"
 /sex="female, virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 213 a 193 c 192 g 177 t

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
9.13e-109	1049.00	92.83%	86.50%	77.19%	775	205	15	3	0	0

US-09-899-634C-2 (1-261) x B1687131 (1-775)

Qy	1	MetAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	20
Db	70	ATGGCGGCGCTACGTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG	129
Qy	21	SerTleThrTrrProGtYGlnMetTleGtYValYValYValYValYValYValYVal	40
Db	130	AGCATCTACTACCCGGAACAGAGATCGAAAGGCCAAAGGGAAGTGGGTATCTACCA	189
Qy	41	CysArpTherLeuGtYProGtYAspGlnGtYProLeuAspTleGtYTrPLeuLeuSer	60
Db	190	TGCAAGTTTACTCTCACTCCGGAAGACCA-GAACCTGACATTTGAATGCTGATATCC	248
Qy	61	ProAlaAspAngTlnYValYsArGtYValYsArGtYValYsArGtYValYsArGtY	80
Db	249	CCGCTGATACACGAGATGATGATATATTTGATTTCTGAGACAAATTTAT	308
Qy	81	AspAspTrrTrrGtYAspLeuYsGtYArYValYHisPheTrrSerAsnAspLeuYsSer	100
Db	309	GATAACTACTATCCGATCTGAAAGACCGGGTACATTTTACGATTAAGATGTCAGTCT	368

QY 101 GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTygIleCys 120
Db 369 GCGGACGACATCTATAATGATGACCACTGACAGTGTGGACATTGGCACTTACCAAGTGC 428
QY 121 LysValIleValIleProGlyValIleGlyAsnIleValIleGlnLeuThrValLeuLeuLys 140
Db 429 AAGTGAAGAAACCCCTGGGGTTCGAAATGAAGAAATTCCTGCTGACCGTCTTGTGTTAAG 488
QY 141 ProSerGlyThrArgCysTyrrValAlaAspGlySerGlnGluIleGlyAsnAspPheLysLeu 160
Db 489 CCTTCAGGTCAAGATGCTTGTGGATGATCGAGAGATGAGAAATGACTTCAAGCTA 548
QY 161 LysCysGluProLysGlnGlySerLeuProLeuLeuLysIleGluThrGlnLysLeuSerAsn 180
Db 549 AATATGAAACCAAGAGAGGCTCCCTTCCACTACAGTTGAATGGAGAAAGTGTGGAC 608
QY 181 SerGlnLysLeuProThrLeuThrLeuAla-GluMetThrSerProValIleSerValIly 200
Db 609 TCCCAACACATGCTTACGCGCATGCTGGCAGCAAAATGACCTCACAGTTATATCTGTGA 668
QY 200 AsnAlaSer-ThrGluTyrrSerGlyThrTyrrSerCysThrValLysAsnArgValGlyS 220
Db 669 GAACGCCAGTTCTGAGTATTCGGGACATACAGCTGCACGATTCAAAACAGAGTGGGCT 728
QY 220 exAspGlnCysLeuLeuArgLeuAspValValProProSerAsnArg 235
Db 729 CTGACCAAGTGTATGCTGCGACCTAGACGTTCTCCACCCCTCAACCGA 775
RESULT 10
BI080376 779 bp mRNA linear EST 20-JUN-2001
LOCUS 602876828F1_NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5008543 5',
DEFINITION mRNA sequence.
ACCESSION BI080376
VERSION BI080376.1 GI:14498706
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 779)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM1053 row: 9 column: 08
High quality sequence stop: 767.
Location/Qualifiers
1..779
/organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5008543"
/clone_1ib="NCI CGAP Mam2"
/cistype="tumor_biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

Alignment Scores:

Pred. No.: 2,39e-105 Length: 779
Score: 1019.00 Matches: 202
Percent Similarity: 92.02% Conservative: 17
Best Local Similarity: 84.87% Mismatches: 14
Query Match: 74.98% Indels: 5
DB: 13 Gaps: 0

US-09-899-634c-2 (1-261) x BI080376 (1-779)

QY 1 MetAlaLeuLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerLeu 20
Db 74 ATGGCGCGCTACTGTGCTTGTGCTTGTGCTTGTGCTGCGGATTCACAGTGGTTTG 133
QY 21 SerIleThrThrProGlnGlnMetIleGluValAlaValGlyGluThrAlaTyrrLeuPro 40
Db 134 AGCATCACTACACCCGACAGAGATCGAAGAAAGGAGGAACTGGCTATCTACCA 193
QY 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluThrLeuLeuSer 60
Db 194 TGCAGTTTACTCTCAGTCCCGAAGACAGGAGCCACTGGACATTGAATGGCTGATATCC 253
QY 61 ProAlaAspAsnGlnLysValAlaAspGlnValIleIleLeuTyrrSerGlyAspLysIleTy 80
Db 254 CGCTCGATTAACCAAGATGATGATCAAGTATCATTTTATTTCTGAGACAAATTTAT 313
QY 81 AspAspTyrrThrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
Db 314 GATTACTACTATCCGATCTGAAAGGACGGGTATTTACAGTAACATGTCAGTCT 373
QY 101 GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTygIleCys 120
Db 374 GCGGACGACATCTATAATGATGACCACTGACAGTGTGGACATTGGCACTTACCAAGTGC 433
QY 121 LysValIleValIleProGlyValIleGlyAsnIleValIleGlnLeuThrValLeuLeuLys 140
Db 434 AAGTGAAGAAAGCCCTGGGGTTCGCAAAATGACCTGACCGTCTTGTGTTA 493
QY 140 sProSerGlyThrArgCysTyrrValAspGlySerGlnGluIleGlyAsnAspPheLysLeu 160
Db 494 GCTTCAAGTACAAAGTGTGCTGATGATCGAAGAGATTGCAATGATTTCAAGC 553
QY 160 eulLysCysGluProLysGlnGlySerLeuProLeuLeuLysIleGluThrGlnLysLeuSer 180
Db 554 TAAATGTAAACCAAGAGAGGCTCCCTTCCACTACAGTTGAATGCGCAAACTGTGG 613
QY 180 snSerGlnLysLeuProThrLeuThrLeuAla-GluMetThrSerProValIleSerVal 199
Db 614 ACTCCAGACAAATGCTTACGCGCATGCTGGCAGCAAAATGACCTCACAGTTATATCTGTG 673
QY 200 LysAsnAlaSer-ThrGluTyrrSerGlyThrTyrrSerCysThrValLysAsnArgVal-GI 219
Db 674 AAGAAAGCCAGTTCTGAGTATTCGTGGACATACAGTGCAGGTTCAAAACGAGTGGG 733
QY 219 ySerAsp-GlnCysLeuLeuArgLeuAspValValProProSer 233
Db 734 CTCTGAACCAAGTGTATGCTGCCACTAGACGTTGTCTCCACCTTCC 777
RESULT 11
AL555497 885 bp mRNA linear EST 16-FEB-2001
LOCUS AL555497 LRI_NFL006_PL2 Homo sapiens cDNA clone CSDDK008Y07 5
DEFINITION prime, mRNA sequence.
ACCESSION AL555497
VERSION AL555497.1 GI:12897284
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 885)
REFERENCE Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
AUTHORS Full-length cDNA libraries and normalization
TITLE

JOURNAL Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.

FEATURES Location/Qualifiers

source

1. .885
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS00K008P07"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 272 a 182 c 190 g 237 t 4 others

ORIGIN

Alignment Scores:

Pred. No.: 8,45e-105 Length: 885
Score: 1015.00 Matches: 191
Percent Similarity: 93.95% Conservative: 11
Best Local Similarity: 88.84% Mismatches: 13
Query Match: 74.69% Indels: 0
Gaps: 9

US-09-899-634c-2 (1-261) x AL555497 (1-885)

47 ProGUaspGinglyProLeuaspIleGluTrpLeuSerProAlaaspAsnGlu 66
6 CCCGAAACGACGAGCCGTCGACATCGATGCTGATATCACCAGCTGATATCAGAAG 65
67 ValaspGlnValIlelleLeuTySerGlyaspIleTyraaspTyTyGlnasp 86
66 GTGATCAAGATGATATTTATTTATCTTGGAACAATAATTAATGATGATATTCAGAT 125
87 LeuaspGlyArGValHisPheThrSerAsnaspLeuysSerGlyaspAlaSerIleasn 106
126 CTGAAAGCCGAGACATTTTACAGATATATCTCAATCTGATGATCAATTAAT 185
107 ValThrAsnLeuGlnLeuSeraspIleGlyThrTyGlnCysValIlyValaPro 126
186 GTAACGAATTTACAACTGTCAGATATTCGACATATCAGTCAAAAGTAAAGTCTCT 245
127 GlyValGlyAsnIlyIleGlnLeuThrValIleuLeuysProSerGlyThrArgCys 146
246 GGTGTTCACAATTAAGAAGATTCATCTGTGATCTTGTAAAGCCCTTCAAGTGCAGATGT 305
147 TyraIaspGlySerGluGluIleGlyAsnaspPheIlyLeuysCysGluProIyGlu 166
306 TACCTTATGATCTGAAAGAAATTCGAAGTCACTTAAAGATTAATGTAACCAAAAGAA 365
167 GlySerLeuProLeuLeuTyGluTrpGlnIlyLeuSerAsnSerGlnIlyLeuProThr 186
366 GGTTCACCTTCATACAGTATGAGTGGCAAMATTGCTGACTCAGCAAAATGCCACT 425
187 LeuTrpLeuAlaGluMetThrSerProValIleSerValIlyAsnAlaSerThrGluTy 206
426 TCATGGTTAGCAGAAATGACTTCACTCTTATCTGTMAAAVATGCTCTTCAGAGAC 485
207 SerGlyThrTySerCysThrValIlyAsnArgValGlySeraspGlnCysLeuLeuArg 226
486 TCTGGACATACAGCTGACGTCAGAAACAGAGGGGCTGATCAGTGGCTGTGGT 545
227 LeuaspValValProProSerAsnArgIleGlyThrIleAlaGlyAlaValIleGlyVal 246

Db 546 CTAACGTTGTCCCTCTTCAATAAAGCTGAGCTAATTGCMGAGCCATTATAGAACT 605

Qy 247 LeuLeuAlaLeuValIleuIleGlyLeuIleIlePheCysCysArg 261

Db 606 TTCTTGCTCTACCGCTCATGTGCTTATCATCTTTGCTGTCT 650

RESULT 12

BM537136 680 bp mRNA linear EST 20-FEB-2002
LOCUS ha78e07.g1 Canis CDNA from testes cells Canis familiaris CDNA
DEFINITION clone ha78e07 5', mRNA sequence.

BM537136 GI:18817097

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 680)
O'Shaughnessy,A.L., McCombie,W.R., Baker,J.P., Balija,V., Cummins
Kirchoff,K.A., Miller,B., Muller,S., Nascimento,L.U., Palmer,L.,
Santos,L., Shah,R.S., Spiegel,L.A., Zucavern,T., Preston,R. and
Hannon,G.J.
Expressed sequence tags from Canis familiaris (dog) (2002)
Unpublished (2002)
Contact: W. Richard McCombie
Iltia Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: ha78 row: e column: 07
Seq primer: -21M13univRev
High quality sequence stop: 680.
Location/Qualifiers

FEATURES

source

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/clone_lib="Canis CDNA from testes cells"
/tissue_type="testes"
/note="Vector: Lambda Zap II; The library was produced by Greg Hannon and Raymond Preston (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using strategene zap cDNA synthesis kit. It was made from dog testes. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."

BASE COUNT 206 a 155 c 151 g 168 t

ORIGIN

Alignment Scores:

Pred. No.: 9.72e-104 Length: 680
Score: 1004.00 Matches: 191
Percent Similarity: 95.15% Conservative: 5
Best Local Similarity: 92.72% Mismatches: 10
Query Match: 73.88% Indels: 0
Gaps: 13

US-09-899-634c-2 (1-261) x BM537136 (1-680)

Qy 1 MetAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuValAlaaspLeuThrArgSerLeu 20
61 ATGGCGCTCTGCTGGCTTCTGCTCTCTGTCGAGATTCACCAAGATTG 120
21 SerIleThrThrProGluGlnMetIleGluValAlaIlyGlyIleThrAlaTyIlePro 40
121 AGATCACTCTCTCTTAACGATGATTTGAAAGCCAAAGGGAATCTTATTTC 180
41 CysArgPheThrLeuGlyProGluaspGinglyProLeuaspIleGluTrpLeuLeuSer 60
181 TGCAAATTTACCTTGTAGTCCAGAAACAGAGGAGCCCTGACATCAGTGGCTGTCTCA 240

OY	61	ProAlaAspAsnGlnLysValAspGlnValIleIleLeuTyrSerGlyAspLysIleTyr	80
Db	241	CCAGTGATTAATCAGAAAGGTGACCAAGTGAATTTATTTATTTCTGGACCAAAATTTAT	300
OY	81	AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer	100
Db	301	GACGACTCTACTCAAGATCTGAAAGAGCAGATACATTTTACAAGCAATGATCTCAATCT	360
OY	101	GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys	120
Db	361	GGTATGATCCATTAATGTATACCAATTTACGGTGTGCAGATATGGCACAATACAGATGC	420
OY	121	LysValLysLysAlaProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLysLys	140
Db	421	AAAGTGAAAAAAGCTCCTGGTGTGGAAATAAGAAATTCACTGACAGTCTTGTGTAAG	480
OY	141	ProSerGlyThrArgCysTyrValAspGlySerGluGluIleGlyAsnAspPheLysLeu	160
Db	481	CCTTCAGGTATTAAGATGTTACCTTATGATGATCAGAAAGAAATGCAATCATTTAAACTA	540
OY	161	LysCysGluProLysGluGlySerLeuProLeuLeuTyrGluThrGlnLysLeuSerAsn	180
Db	541	AAATGTGAACCAAAAGAAAGTTCACTTCATTACAATATGAATGGCAAAAATTTGCCAT	600
OY	181	SerGlnLysLeuProThrLeuThrLeuAlaGluMetThrSerProValIleSerValLys	200
Db	601	TCACAGAAAACGCCCCCTCGGTGCACACAGATATGACTTCACCTGTGTATCATATAAA	660
OY	201	AsnAlaSerThrGluTyr	206
Db	661	AAATGCTCTACTGAGGTAC	678

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RESULT 13
BI823597
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM11453 row: j column: 16
High quality sequence stop: 705.
location/Qualifiers
1..885

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/db xref="taxon:9606"
/clone="IMAGE:5181807"
/clone.lib="N1H MGC_115"
/lab host="DH10B"
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pCMV-SPORT6; site_1: NotI; site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27, and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,

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BASE COUNT	ORIGIN
263 a	191 c 216 g 215 t

insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MGC Library."

Alignment Scores:	
Pred. No.:	1.08e-95
Score:	935.00
Percent Similarity:	84.56%
Best Local Similarity:	79.15%
Query Match:	68.80%
DB:	13
	Length: 885
	Matches: 205
	Conservative: 14
	Mismatches: 28
	Indels: 14
	Gaps: 4

Oy	1	Met1a1euleuleu	CysPheVal1euleu	CysGlyVal1a1aAspLeuThrArgSer	20
Db	77	ATGGCGCTCC	CGCTGCTGCTCTCTCTCGTGGGAGT	AGTGGATTTCGCCAGAAGTTG	136
Oy	21	Ser1LeThrThr	ProGluGluMet1	IleGluVal1a1aGlyGluThrAla1	ThrLeuPro 40
Db	137	AGTATCACTAC	TCTCTGGAAGACATATTGAAAAACCCAAAGGGAAAC	TGGCTATCTGGCA 196	
Oy	41	CysArgPheThrLeu	GlyProGluAspGlnGlyProLeuAsp1	IleGluThrLeuLeuSer 60	
Db	197	TGCAAAATT	TACGCTTAATGTCGCCGAAGACCA -GACCCGCTGGACATCGAGTGTATATCA 255		
Oy	61	ProAlaAsp	AsnGlnVal1a1aIleLeuThrSerGlyAsp	LeuPheTyr 80	
Db	256	CCACCTGATAT	ATCAGAAGGTGATCAAGTATTTTATTTATTTCTGGGACAAATAATTAT 315		
Oy	81	AspAsp -Tyr	ThrClnAspLeuLeuSerGlyArgValHisPhe	ThrSerAsnAspLeuValSer 100	
Db	316	GATACCTGACTAT	CACAGTCTGAAAAGCCGAGTACATTTTACGATATGATCTCAAAATC 375		
Oy	100	rg1Asp	AlaSer1IleAsnValThrAsnLeuGlnLeuSerAsp1	IleGlyThrTyrGlnCys 120	
Db	376	TGGTGATGCAT	CATTAATGTAAATGTAACGAATTTTACACTGTCAGATTTGGCATATATCAATGTCAGTG 435		
Oy	120	gLyVal1	LeuVala1aProGlyVal1GlyAsnLeuVal1	IleGluThrVal1LeuLeuVal 140	
Db	436	CAAAAGTAAAA	AAAGCTCCTGGTGTGCAAAATMAAAGATTCAATCTGTAGTCTTGTTAA 495		
Oy	140	sProSerGlyThr	ArgCysTyrVala1aAspGlySerGluGluIleGlyAsnAspPhe	ValSerLe 160	
Db	496	GCCTTCAGGTG	CCGAGATGTTACGTTGATGATCTGAAAGAAATTGGAGTCACTTAAAGAT 555		
Oy	160	uLyCysGlu	ProLysGluGlySerLeuProLeuLeuTyrGluThrGln	ValLeuSerAs 180	
Db	556	AAATGTGAAC	CCAAAGAGGTTCACTTCCATTCACAGATGAGTGGCAAAATATGCTGCA 615		
Oy	180	nSerGln	LeuLeuProThrLeuThrPheAlaGlu-MetThrSerPro	Val1IleSerVal 200	
Db	616	CTCACAGAAAT	TGCCACTTCATGATGTTACGAAACATGACTTCAATCTGTCAATATCTGTTA 675		
Oy	200	ysAsnAla	SerThrGluTyrSerGlyThrTyrSer -CysThr	ValLys--AsnArgVal 218	
Db	676	AAATATGC -TCT	TTCGAGTACTCTGGGACATATCACTTGTACCGCTCGAAGAACAGAAAGG 734		
Oy	219	Gly-----	SerAspGlnCys--LeuLeuArgLeuAsp	ValValProProSer 233	
Db	735	GGAAGCTCAT	GATCTCCAGTGCATATGGCGTTTAAAGCGTTGCTGCCCTCTT -TCA 788		
Oy	234	Asn -Arg	AlaGly1Thr1IleAlaGlyAlaVal1IleGlyVal1	LeuLeuAla 249	
Db	789	AATCAAA	GCTGGACTAATTGGACAGACCTTATTAAGAACTTGCTGGCA 837		

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 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
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 1 (bases 1 to 702)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgsab-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
 Plate: L14M1047 row: a column: 07
 High quality sequence, stop: 700.
 Location/Qualifiers
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 /clone_1lb="NCT CGAP Mam2"
 /tissue_type="tumor, biopsy sample"
 /dev_stage="5 months"
 /lab_host="MDH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
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 Percent Similarity: 91.47% Conservative: 13
 Best Local Similarity: 85.31% Mismatches: 16
 Query Match: 67.22% Indels: 3
 Gaps: 1
 DB: 13
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 71 ATGGCGGCGCTACTGCTGCTTCTTGGCGGATCGGATTTTACCAGTGGTTG 130
 21 SerIleThrThrProGluGlnMetIleGluLysAlaLysGluThrAlaTyrLeuPro 40
 131 AGCATCACTACACCGCAAGAGATCGAAAGGCAAGGGAAGTGGTACTTACCA 190
 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluTyrLeuLeuSer 60
 191 TGCAAGTTTACTCTCAGTCCGAAAGACCA-GGACCACATGGAATGCTGATATCC 249
 61 ProAlaAspAsnGlnLysValAspGlnValIleIleLeuTyrSerGlyAspLysIleTyr 80
 250 CCGTGTGATTAACCGATATGATGATCAATGATTCATTGTCGAGACAAATTTAT 309
 81 AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
 310 GATTAACACTACTCCGATCTGAAAGGACGGGTACATTTTACAGAAAGATGCAAGTCT 369
 101 GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys 120
 370 GGCAGCGATCTATTAATGATGACCACTGACAGTGTGAGCAATTGGCACTTACCACTGCTC 429

121 LysValLysLysAlaProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLys 140
 430 AAAGTGAAGAAAGCCCTGGGGTTCAGAAATTAAGAAATCTGCTGACCGTTCTTTAAG 489
 141 ProSerGlyThrArgCysTyrValAspGlySer---GluGluIleGlyAsn-AspPheIy 159
 490 CTTTCAGTTCAGAAATGCTTCGGAAGATCGGCACACAGATTGGAAACTGACTTCAA 549
 159 SLeuLysCysGluProLysGluGlySerLeuProLeuLeuTyrGluTyrGlnLysLeuSe 179
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 179 AsnSerGlnLysLeuProThrLeuThrLeuAlaGluMetThrSerProValIleSerVa 199
 610 GCACTCCACACAAATGCTACGCGATGCGGCAAGAAATACGTCACAGTTATATCTGT 669
 199 LysAsnAlaSerThrGluTyrSerGlyThr 209
 670 GAAGAACGCGAGTCTGAGTATCTGGGACA 700
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 ACCESSION AL514786
 VERSION AL514786
 KEYWORDS AL514786.1 GI:12778279
 SOURCE EST.
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 838)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (2001)
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@life.com URL : http://fulllength.invitrogen.com"
 BASE COUNT 239 a 191 c 197 g 207 t 4 others
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 Pred. No.: 7.87e-93 Length: 838
 Score: 909.50 Matches: 180
 Percent Similarity: 81.51% Conservative: 14
 Best Local Similarity: 75.63% Mismatches: 30
 Query Match: 66.92% Indels: 15
 Gaps: 2
 DB: 9
 US-09-899-634c-2 (1-261) x AL514786 (1-838)
 1 MetalauleuLeuCySpheValleuLeuCySgiValAlaapLeuThrArgSerleu 20


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Db      67  ATGGCGCTCCTGCTGCTGCTTCTGCTCTCTGCGGAGTAGTGATTTCCGACAGATTG 126
QY      21  SerIleThrThrProGluGlnMetIleGluLysAlaLysGluThrAlaTyrLeuPro 40
      127  AGTATCACTACTCTCTGAGAGATGATGAAAAAGCCAAAGGGAACTGCCTATCTGCCA 186
QY      41  CysArgPheThrLeuGluProGluAspGlnGlyProLeuAspIleGluTyrPheLeuSer 60
      187  TGCAAATTACGCTTACTCTCCGAGACACAGGAGCCCTGACATCGAGTGGCTGATATCA 246
QY      61  ProAlaAspAsnGlnLysValAspGlnValIleIleLeuTyrSerGlyAspLysIleTyr 80
      247  CCAGCTGATATATCAGAAAGTGATGATCAAGATATTTATTTCTGAGACAAAATTAT 306
QY      81  AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
      307  GATGACTACTATCCAGATCTGAAAGCCGAGTACATTTTACGAGTTATGATCTCAAAATCT 366
QY      101  GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys 120
      367  GGTGATGACATCAATAATGATGACAAATTTCACAACTGTCAGATATTGGCACATATCAGTGC 426
QY      121  LysValLysLysAlaProGluValGlyAsnLysIleGlnLeuThrValLeuLeuLys 140
      427  AAAGTGAAAAAGCTCTGAGTGTGCAAAATGAGAGATTCATCTGTAGTCTTGTTAG 486
QY      141  ProSerGlyThrArgCysTyrValAspGlySerGluGluIleGlyAsnAspPheLysLeu 160
      487  CCTTCAGGTGCGAGATGTTTCGTTGATGAGTCTGAAGAAATTGGAAGTGACTTTAGATA 546
QY      161  LysCysGluProLysGluGlySerLeuProLeuLeuTyrGluTyrGlnLysLeuSerAsn 180
      547  AATATGGAACCAAAAGAGGTTCACTTCATTCAGATGAGTGGCAAAAATTGTCTGAC 606
QY      181  SerGlnLysLeuProThrLeuTyrPheAla---GluMetThrSerProValIleSerVal 199
      607  TCACAGAAATATGCCCACTTATGTTAGCAGGAGAGATGTG-CCACCTCCAAAGAGCGCT 665
QY      200  LysAsnAlaSerThrGluTyrSerGlyThrTyrSerCysThrValLysAsnArgValGly 219
      666  ACGTCCACTGCCAGAGCTACATCGGCGATTATCATTCATC----- 707
QY      220  SerAspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGly 237
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Job time : 1110 secs

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